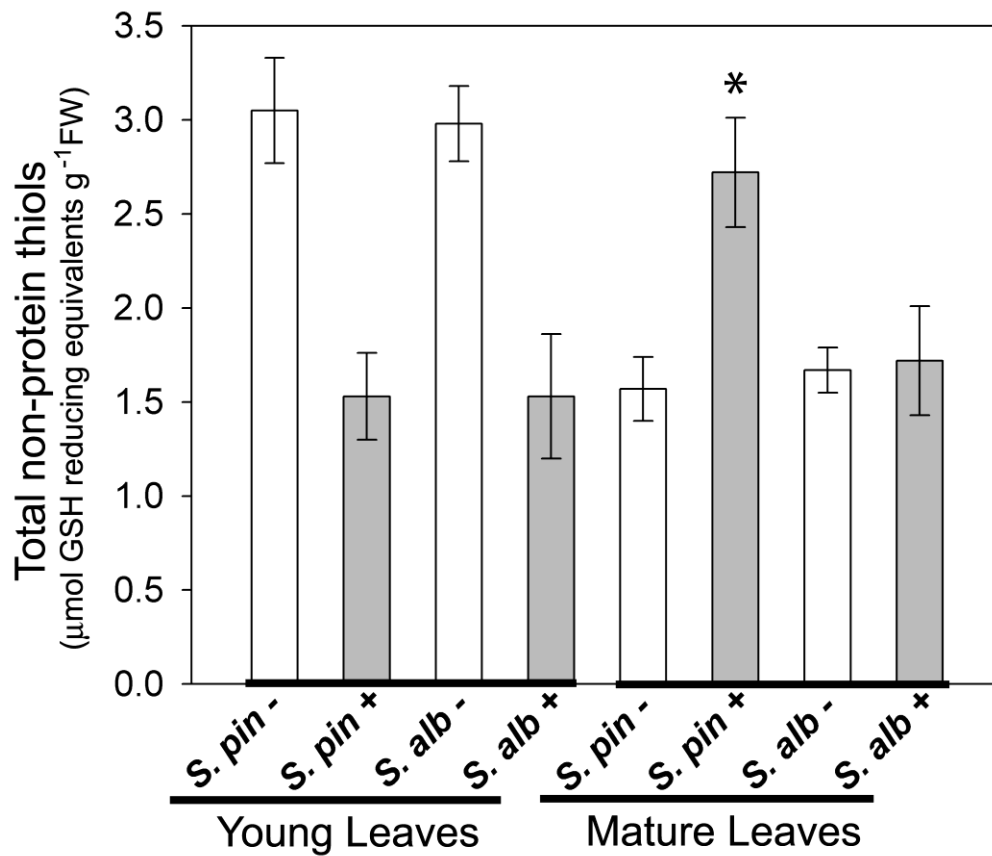
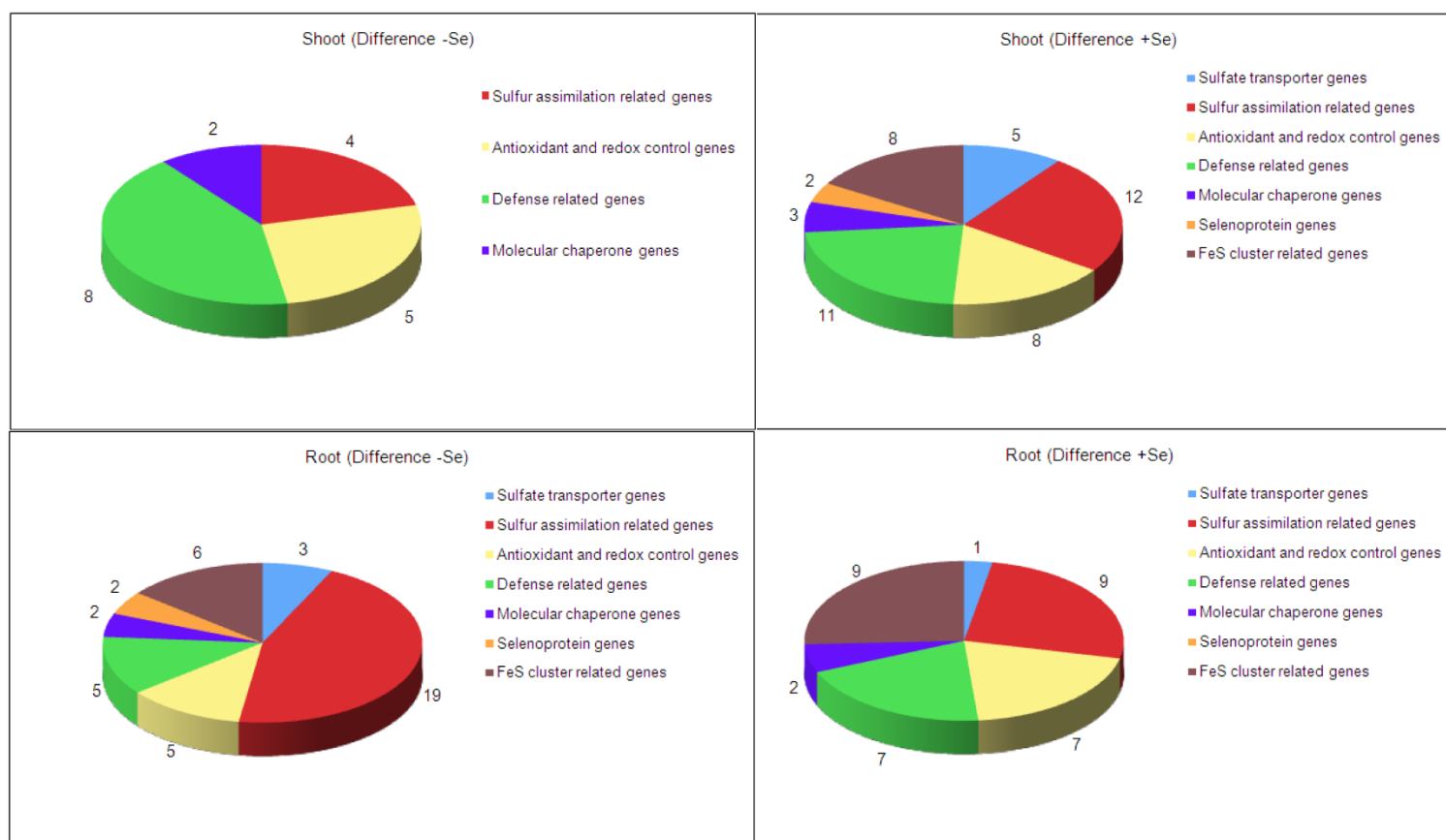


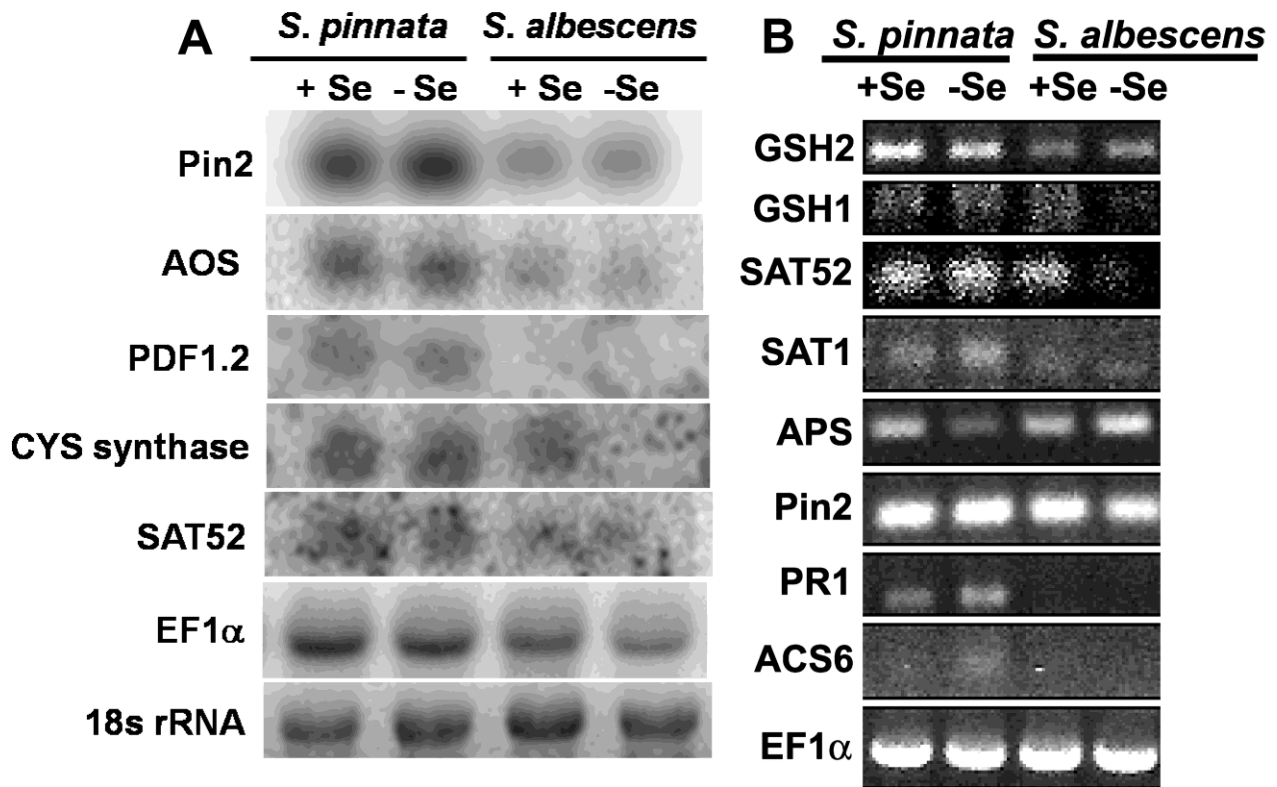
Supplemental Figure 1. Root lengths of *S. pinnata* and *S. albescens* grown on vertically placed agar plates after 30 days of growth from germination. Plants treated without (–) Se (open bars) and with (+) 20 μM SeO_4^{2-} (gray bars). Data represent the average of 4-5 different plants \pm SE. P-values using a student's *t* test are reported in paragraph 1 of results section.



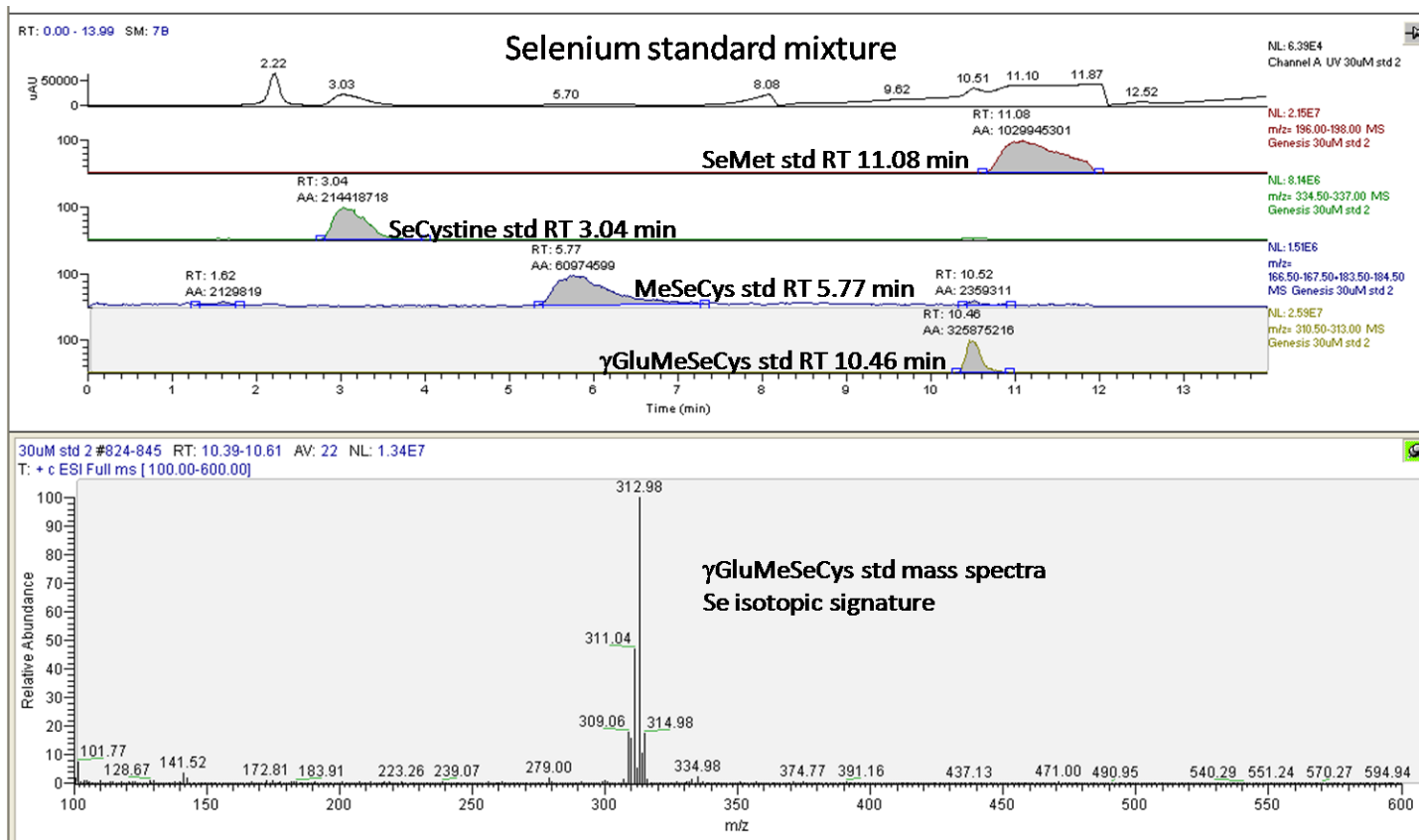
Supplemental Figure 2. Total non-protein thiols expressed as GSH equivalents ($\mu\text{mol g}^{-1}$ fresh weight) in young and mature leaves of *S. pinnata* and *S. albescens* grown with or without $20 \mu\text{M SeO}_4^{2-}$. The only significant difference between treatments in comparison to the other species using a student's *t* test ($P < 0.05$) is denoted with an asterisk.



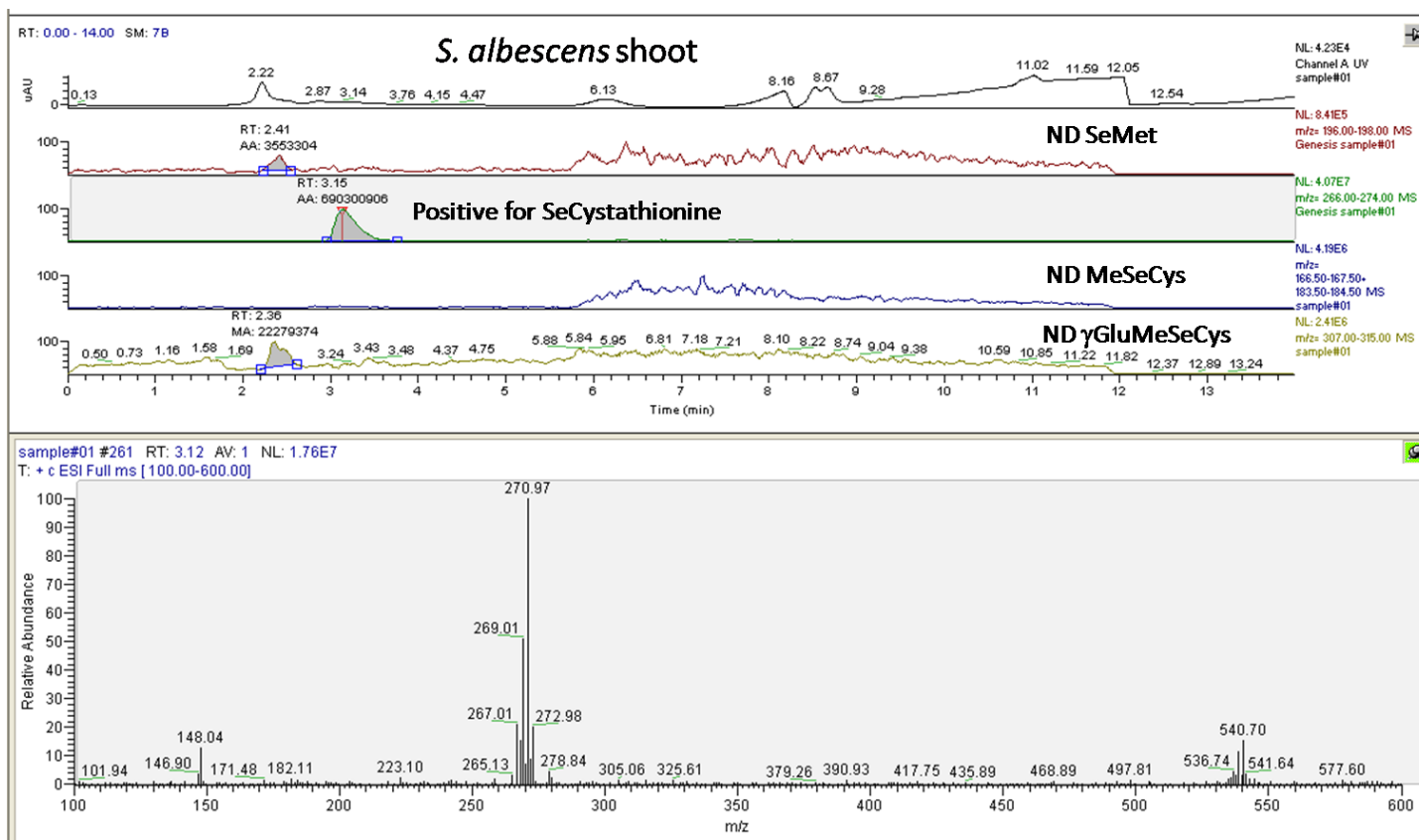
Supplemental Figure 3. Graphic depiction of the macroarray expression differences from Tables 1-4 and the relative numbers of genes in different categories in young leaves (shoots) and roots of 10-week old *S. pinnata* when compared with *S. albensens* grown with and without 20 μ M SeO₄²⁻.



Supplemental Figure 4. Northern Blot and Semiquantitative RT-PCR confirms the gene expression patterns identified in macroarray analysis using a select set of *A. thaliana* probes for genes that showed differences in the macroarray studies. Three genes associated with pathogen defense (*Pin 2*, *AOS* and *PDF 1.2*) and two genes involved in cysteine biosynthesis (*CYS synthase* and *SAT52*) were all normalized to control *EF1 α* (Supplemental Figure 4A). RT-PCR used a select set of *A. thaliana* primers for genes involved in sulfur metabolism, GSH biosynthesis and pathogen defense that showed differences in the macroarray studies. *EF1 α* is used as a constitutive control for RT-PCR (Supplemental Figure 4B). Messenger RNA was isolated from young leaves of 10-week old *S. pinnata* and *S. albescens* with and without 20 μM SeO_4^{2-} . Results quantified using image J are presented in supplemental table 4.



Supplemental Figure 5 A.



Supplemental Figure 5 B.

Supplemental Figure 5. A) Liquid chromatographic separation of four authentic seleno-amino acid standards. Mixture of selenomethionine, selenocystine, methylselenocysteine, and γ -glutamyl-methylselenocysteine. Mass spectra for γ -glutamyl-methylselenocysteine (gGluMeSeCys) shown with the correct Se isotopic signature. B) Positive mass spectra for Selenocystathionine (SeCyst) with the correct Se isotopic signature. SeCyst is the only free organic selenium compound detected in *S. albenscens*, n=3 different plants, young and old leaves. Also not detected (ND) selenocysteine and selenocystine, negative data not shown.

Supplemental Table 1.			
Gene set 1	Shoots	Fold induction by selenate	
AGI code	Annotation	<i>S. albenscens</i>	<i>S. pinnata</i>
At1g67810	CpSufE2	1.09	1.51
At5g50210	CpSufE3	1.17	1.36
At4g04770	CpSufB	1.50	1.69
At3g10670	CpSufC	1.35	1.99
At1g32500	CpSufD	1.09	2.22
At3g24430	HCF101	1.10	2.02
At1g64810	APO1	1.41	1.00
At1g03850	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	1.25	2.60
At1g32760	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	0.91	0.73
At2g20270	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	1.00	1.50
At2g38270	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	1.06	1.71
At2g41330	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	1.09	1.66
At3g15660	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	0.91	1.38
At3g54900	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	1.45	3.65
At3g57070	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	1.14	2.52
At4g28730	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	1.35	1.65
At5g11930	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	2.51	1.40
At5g13810	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	1.37	3.17
At5g58530	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	1.61	1.15
At3g62930	glutaredoxin affected by Se, cellular component unknown, arsenate reductase (glutaredoxin) activity, electron transport, thiol-disulfide exchange intermediate activity	0.90	2.34
At1g28480	glutaredoxin affected by Se, electron transport, jasmonic acid mediated signaling pathway, salicylic acid mediated signaling pathway, thiol-disulfide exchange intermediate activity, response to salicylic acid stimulus	0.76	1.55
At5g04590	SIR (sulfite reductase, plastid, sulfite reductase activity, sulfate reduction	0.72	1.38
At2g15620	nitrite reductase	0.52	1.33
At1g10960	ferredoxin	1.05	2.28
At1g32550	ferredoxin	1.52	1.38
At2g27510	ferredoxin	1.44	0.82
At1g60950	ferredoxin	1.10	1.59

AtCg00350	PsaA/B	0.23	1.05
AtCg01060	PsaC (chloroplast thylakoid membrane, electron carrier activity, iron ion binding	1.31	2.55
At5g04140	glutamate synthase, ferredoxin dependent glutamate synthase (Fd-GOGAT). Expression in leaves is induced by light and sucrose. Proposed to be involved in photorespiration and nitrogen assimilation.	2.56	4.63
At4g03280	Rieske protein involved photosynthetic electron transport cytochrome b6/f, nonphotochemical quenching, encodes the FeS center of cytochrome b6f complex	6.98	2.53
At4g29890	choline monooxygenase	1.01	2.88
At4g34740	Amidophosphoribosyltransferase	0.89	1.89
At3g23940	Dihydroxy-acid dehydratase	0.93	1.33
At2g04700	Ferredoxin-thioredoxin reductase	1.01	1.76
At1g45904	NADH-plastoquinone oxidoreductase	0.79	1.19
AtCg01090	subunit I (NdhI)	0.90	0.93
At3g44880	Pheophorbide a oxygenase (LLS1)	1.06	1.02
At1g50170	Sirohydrochlorin ferrochelatase	0.80	0.93
At2g24820	Tic55, plastid protein import	1.09	2.43
At4g25650	Tic55, plastid protein import	1.15	2.35
At1g03130	PsaD	1.39	4.56
At1g67090	Rubisco SSU	1.06	2.26
At4g34900	xanthine dehydrogenase	0.72	2.07
At2g31955	xanthine dehydrogenase	0.75	1.55
At2g43360	biotin synthase	0.69	1.02
At2g25080	GSH peroxidase chloroplast, glutathione peroxidase activity, response to oxidative stress	0.85	2.66
At2g31570	GSH peroxidase	0.59	1.76
At3g54660	glutathione reductase (GR)	1.47	1.86
At3g03780	methionine synthase cytosolic	1.39	1.33
At5g17920	methionine synthase cytosolic	1.48	1.08
At5g20980	methionine synthase chloroplastic	0.93	1.11
At5g49810	methionine methyl transferase	1.01	1.23
At1g64280	NPR-1	1.04	1.53
At1g56600	GalactinolSynthase 2 (water stress related protein, carbohydrate biosynthetic process transferase activity, transferring hexosyl groups, transferase activity, transferring glycosyl groupsgalactinol synthase-like protein [Thellun (GB:AAM19710.1); contains InterPro domain Glycosyl transferase, family 8; (InterPro:IPR002495) water stress related protein carbohydrate biosynthetic process transferase activity, transferring hexosyl groups, transferase activity, transferring glycosyl groups	0.49	3.61
At5g43840	HSP TF	0.81	1.47
At1g05680	auxin signaling	0.77	1.06
At1g02850	glycosyl transferase	0.83	0.92
At4g11650	osmotin	0.81	1.44
At2g29490	GSH transferase, toxin catabolic process located in cytoplasm has glutathione transferase activity	0.96	2.02
At5g12030	HSP 17.6	1.28	1.85
At5g52300	response to water deprivation, response to salt stress, response to abscisic acid stimulus, The promoter region contains two ABA-responsive elements (ABREs) that are required for the dehydration-responsive expression of rd29B as cis-acting elements.	1.21	2.37
At5g13170	nodulin MtN3 family protein; similar to MTN3, senescence protein	0.95	2.40
At1g23730	carbonic anhydrase, carbon utilization, functions in zinc ion binding, has carbonate dehydratase activity	1.19	2.40

At3g01500	carbonic anhydrase chloroplast thylakoid membrane, carbonate dehydratase activity, zinc ion binding, carbon utilization	1.79	3.61
At3g51860	Ca/H antiporter	0.72	1.16
At3g63440	cytokinin oxidase	0.90	1.42
At5g44120	legumin-like protein	0.53	2.93
At5g38710	proline oxidase	0.80	1.68
At4g34410	ERB (ethylene receptor) TF	0.68	1.17
At1g12610	Cold binding factor 1 TF	0.71	0.98
At5g12020	HSP 17.6	0.69	1.57
At4g33720	PR (pathogenesis-related protein, putative; similar to ATPRB1 (Arabidopsis thaliana basic pathogenesis-related protein 1))	1.04	4.48
At2g26150	HSP TF	1.37	1.37
At3g46230	HSP17 involved in response to heat, member of the class I small heat-shock protein (sHSP) family, which accounts for the majority of sHSPs in maturing seeds	1.23	3.21
At1g59860	HSP17	0.75	1.91
At1g53540	HSP 17.6	0.86	1.54
At3g12580	HSP70	0.68	1.18
At4g11280	ACC synthase	1.31	1.32
At1g27730	STZ (salt tolerant zinc finger, nucleic acid binding, transcription factor activity, zinc ion binding, response to chitin. Related to Cys2/His2-type zinc-finger proteins found in higher plants. Compensated for a subset of calcineurin deficiency in yeast. Salt tolerance produced by ZAT10 appeared to be partially dependent on ENA1/PMR2, a P-type ATPase required for Li+ and Na+ efflux in yeast. The protein is localized to the nucleus, acts as a transcriptional repressor and is responsive to chitin oligomers.	0.99	2.65
At4g02200	drought induced protein	1.02	1.46
At5g51440	mitochondria HSP	0.78	1.10
At3g08490	Chl a/b binding protein	1.09	0.78
At4g02770	PSI D protein	0.98	1.92
At1g52820	gibberellin oxidase	1.23	1.92
At5g04960	pectinesterase	0.93	1.56
At2g46690	auxin regulated protein	0.86	1.96
At2g34370	putative selenium binding protein(pentatricopeptide (PPR) repeat-containing protein)	0.88	1.09
At4g14040	putative selenium binding protein (56kDa selenium binding protein (SBP56))	0.78	1.44
At4g14030	selenium binding protein (56kDa selenium binding protein (SBP56)) putative function in selenium-binding ; Identical to Putative selenium-binding protein [Arabidopsis thaliana] (GB:O23264); similar to EDA38 (embryo sac development arrest 38), selenium binding [Arabidopsis thaliana] (TAIR:AT4G14040.1); similar to selenium-binding family protein [Arabidopsis thaliana] (TAIR:AT3G23800.1); similar to selenium binding protein [Lotus japonicus] (GB:CAC67491.1); similar to putative selenium-binding protein [Thellun (GB:AAM19706.1); similar to selenium binding protein [Medicago sativa] (GB:CAC67501.1); contains InterPro domain Quinoprotein amine dehydrogenase, beta chain-like; (InterPro:IPR011044); contains InterPro domain Selenium-binding protein; (InterPro:IPR008826)	1.24	2.70
At3g23800	selenium-binding family protein; similar to EDA38, selenium binding [Arabidopsis thaliana] (TAIR:AT4G14040.1); similar to selenium-binding protein, putative [Arabidopsis thaliana] (TAIR:AT4G14030.1); similar to selenium binding protein [Lotus japonicus] (GB:CAC67491.1); similar to selenium binding protein [Glycine max] (GB:CAC67472.1); similar to selenium binding protein [Medicago sativa] (GB:CAC67501.1); contains InterPro domain Quinoprotein amine dehydrogenase, beta chain-like;	0.78	2.03

	(InterPro:IPR011044); contains InterPro domain Selenium-binding protein; (InterPro:IPR008826)		
At2g03880	putative selenium binding protein, pentatricopeptide (PPR) repeat-containing protein; similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:AT3G24000.1); similar to Os06g0472300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001057622.1); similar to PPR986-12 [Physcomitrella patens] (GB:BAD67155.1); contains InterPro domain Pentatricopeptide repeat; (InterPro:IPR002885); contains InterPro domain Protein prenyltransferase; (InterPro:IPR008940); contains InterPro domain Tetratricopeptide-like helical; (InterPro:IPR011990)	0.84	2.01
At2g25580	putative selenium binding protein	0.70	1.13
At5g40415	putative selenium binding protein	0.80	0.92
At5g48910	putative selenium binding protein	0.93	1.82
At1g05720	selenoprotein family protein, contains Prosite PS00190: Cytochrome c family heme-binding site signature; similar to 15 kDa selenoprotein	0.79	1.20
At3g22740	homocysteine S-methyltransferase 3 (HMT-3), identical to homocysteine S-methyltransferase HMT-3 (Arabidopsis thaliana) GI:9966515; similar to homocysteine S-methyltransferase AtHMT-2 (GI:6685163) (Arabidopsis thaliana); similar to selenocysteine methyltransferase GB:P56707 from (Astragalus bisulcatus)	1.10	1.55
At3g47300	selenoprotein-related, contains weak similarity to selenoprotein W	0.96	1.61
At5g58640	similar to selenoprotein-related [Arabidopsis thaliana] (TAIR:At3g47300.1)	1.05	1.54
At1g01910	similar to anion-transporting ATPase family protein	1.04	1.53
At1g08490	AtCpNifS (cysteine desulfurase, putative, similar to nitrogen fixation protein (nifS))	1.12	2.69
At1g10500	AtCplscA (Involved in chloroplast Fe-S cluster assembly. Located in the chloroplast stroma.)	1.38	2.00
At1g16460	ATRDH2 (encodes a cytoplasmic thiosulfate:cyanide sulfurtransferase, activity of which increased the rhodanese activity of transgenic yeast. Can also act as a mercaptopyruvate sulfurtransferase)	0.57	1.67
At1g18490	Chloroplastic NifS-like protein that can catalyze the conversion of cysteine into alanine and elemental sulfur (S(0)) and of selenocysteine into alanine and elemental Se (Se(0)). Overexpression enhances selenium tolerance and accumulation	1.09	3.17
At1g19920	APS2 (sulfate adenylyltransferase 2 / ATP-sulfurylase 2 (ASA1) (MET3-1) (APS2), identical to ATP sulfurylase)	0.81	1.38
At1g30910	molybdenum cofactor sulfurase family protein, weak similarity to molybdenum cofactor sulfurase (LOS5/ABA3)	0.77	0.78
At1g31190	Involved in sulfur metabolic process, inositol or phosphatidylinositol phosphatase activity, located in chloroplast has 3'(2'),5'-bisphosphate nucleotidase activity, inositol or phosphatidylinositol phosphatase activity, inositol monophosphatase family protein, similar to SP P29218 Myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25) (Inositol monophosphatase)	0.89	2.37
At1g51390	NFU5 (nitrogen fixation NifU-like family protein, similar to HIRA-interacting protein 5 (NIFU FAMILY)	1.06	1.79
At1g55880	pyridoxal-5'-phosphate-dependent enzyme, beta family protein, similar to SP P50867 Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) (Aspergillus nidulans) {Emericella nidulans}; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme	1.43	0.85
At1g55920	Serat2;1 (serine O-acetyltransferase, putative, identical to GI:608677 from (Arabidopsis thaliana)	0.89	1.58
At1g62180	APR2 (5'-adenylylsulfate reductase 2, Second enzyme Involved in sulfate reduction, chloroplast (APR2) (APSR) / adenosine 5'-phosphosulfate 5'-adenylylsulfate (APS) sulfotransferase 2 / 3'-phosphoadenosine-5'-phosphosulfate (PAPS) reductase homolog 43 (PRH-43)	1.15	2.22

At1g70560	alliinase C-terminal domain-containing protein, contains Pfam profiles: PF04864 allinase C-terminal domain, PF04863 alliinase EGF-like domain	0.79	1.19
At1g79230	mercaptopyruvate sulfurtransferase (MST1) (RDH1), identical to mercaptopyruvate sulfurtransferase GI:6009981 and thiosulfate sulfurtransferase GI:5834508 from (Arabidopsis thaliana) encodes a sulfurtransferase/rhodanese, which belongs to a group of enzymes widely distributed in all three phyla that catalyze the transfer of sulfur from a donor to a thiophilic acceptor substrate. The protein and transcript levels are NOT affected by senescence or exogenous cyanide, suggesting that sulfurtransferases are involved in cyanide detoxification.	1.05	2.33
At2g14750	AKN1 (adenylylsulfate kinase 1 (AKN1), identical to adenylylsulfate kinase 1, chloroplast precursor (APS kinase, Adenosine-5'-phosphosulfate kinase, ATP adenosine-5'-phosphosulfate 3'-phosphotransferase) (Arabidopsis thaliana) SWISS-PROT:Q43295	0.93	1.32
At2g16710	IscA-like protein (hesB-like domain-containing protein, similar to IscA (putative iron-sulfur cluster assembly protein) (Azotobacter vinelandii) GI:2271523; contains Pfam profile PF01521: HesB-like domain	0.56	1.46
At2g17640	Serat3;1 (serine O-acetyltransferase, putative (SAT-106), similar to Arabidopsis thaliana serine acetyltransferase GI:905391	0.81	1.86
At2g36260	iron-sulfur cluster assembly complex protein, putative, similar to IscA (putative iron-sulfur cluster assembly protein) (Azotobacter vinelandii) GI:2271523; contains Pfam profile PF01521: HesB-like domain	0.88	1.09
At2g43750	Bsas2;1 (cysteine synthase, chloroplast / O-acetylserine (thiol)-lyase / O-acetylserine sulfhydrylase / cpACS1 (OASB), identical to SP P47999 Cysteine synthase, chloroplast precursor (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) (cpACS1) {Arabidopsis thaliana}; identical to cDNA O-acetylserine lyase (At.OAS.7-4) GI:6983575	1.09	1.66
At3g01020	Encodes a mitochondrial protein similar to E.coli IscU. In bacteria, IscU is a scaffold protein accepting sulfur and iron to build a transient Fe-S cluster, which is subsequently transferred to a target apoprotein.	0.85	0.97
At3g02870	inositol-1(or 4)-monophosphatase, putative / inositol monophosphatase, putative / IMPase, putative, similar to SP P54928 Inositol-1(or 4)-monophosphatase 3 (EC 3.1.3.25) (IMPase 3) (IMP 3) (Inositol monophosphatase 3) {Lycopersicon esculentum}; contains Pfam profile PF00459: Inositol monophosphatase family	1.18	2.75
At3g03630	Bsas5;1 (cysteine synthase, chloroplast, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, identical to SP O22682 Probable cysteine synthase, chloroplast precursor {Arabidopsis thaliana}, similar to SP P31300 Cysteine synthase, chloroplast precursor {Capsicum annuum}	0.64	0.34
At3g04940	Bsas4;1 (cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, similar to O-acetylserine(thiol) lyase (EC 4.2.99.8) (Brassica juncea) GI:2245144; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme	0.81	1.22
At3g13110	Serat2;2 (serine O-acetyltransferase (SAT-1), identical to serine acetyltransferase (Sat-1) GI:1184048 (Arabidopsis thaliana)	0.98	1.46
At3g20970	NFU4 (nitrogen fixation NifU-like family protein, similar to HIRA-interacting protein 5 (NIFU FAMILY) (SP:Q9QZ23) {Mus musculus}; contains Pfam profile: PF01106 NifU-like domain	1.07	2.53
At3g22460	Bsas1;4 (Cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, nearly identical over 185 amino acids to SP P47998 Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) {Arabidopsis thaliana}	0.93	2.37
At3g22890	APS1 (ATP sulfurylase, the first enzyme in the sulfate assimilation pathway of Arabidopsis)	1.24	2.58

At3g59760	Bsas2;2 (cysteine synthase, mitochondrial, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, similar to SP Q43725 Cysteine synthase, mitochondrial precursor (EC 4.2.99.8) (O- acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) {Arabidopsis thaliana}	1.07	1.89
At3g61440	Bsas3;1 (encodes a cysteine synthase isomer. The isomer is however less effective in cysteine biosynthesis. It is involved in beta-cyanoalanine biosynthesis, a intermediate of cyanide detoxification pathway.	1.07	1.73
At4g01940	NFU1 (nitrogen fixation NifU-like family protein, similar to apricot NifU homolog partial CDS, GenBank accession number U95179; contains Pfam profile: PF01106 NifU-like domain)	1.18	2.37
At4g04080	Encodes a mitochondrial protein similar to E.coli IscU. In bacteria, IscU is a scaffold protein accepting sulfur and iron to build a transient Fe-S cluster, which is subsequently transferred to a target apoprotein.	0.86	0.88
At4g04610	APR1 (5'-adenylylsulfate reductase (APR1) / PAPS reductase homolog (PRH19), identical to 5'-adenylylsulfate reductase (Arabidopsis thaliana) GI:2738756; identical to cDNA PAPS reductase homolog (PRH19) GI:1710111	1.61	3.46
At4g14880	Bsas1;1 (cysteine synthase / O-acetylserine (thiol)-lyase / O-acetylserine sulfhydrylase (OAS1), nearly identical to SP P47998 Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) {Arabidopsis thaliana}; identical to cDNA O-acetylserine lyase (At.OAS.5-8) GI:6983573	1.37	1.63
At4g21990	APR3 (5'-adenylylsulfate reductase (APR3) Second enzyme Involved in sulfate reduction/ PAPS reductase homolog (PRH26), identical to 5'-adenylylsulfate reductase (Arabidopsis thaliana) GI:2738760; identical to cDNA PAPS reductase homolog (PRH26) GI:1710113	1.45	3.45
At4g22220	ISU1 (iron-sulfur cluster assembly complex protein, putative, similar to iron-sulfur cluster assembly complex ISCU1 (GI:11545705) (Homo sapiens); nifU protein homolog YPL135w (GI:15619823) (Saccharomyces cerevisiae) PIR2:S69049)	0.67	1.12
At4g24670	Allinase family protein, Carbon-sulfur lyase activity, endomembrane system, contains Pfam profiles: PF04864 allinase C-terminal domain, PF04863 allinase EGF-like domain	0.99	2.20
At4g25910	NFU3 (nitrogen fixation protein, putative, nitrogen fixation protein nifU (SP:Q43885) (Anabaena sp.); contains Pfam profile: PF01106 NifU-like domain)	1.00	1.93
At4g26500	AtSufE (Sulfur acceptor that interacts with and activates the cysteine desulfurases, AtSufS in plastids and AtNifS1 in mitochondria, and both activations are vital during embryogenesis. Dual localization in mitochondria and chloroplasts. Involved in Fe-S cluster biogenesis in mitochondria and plastids. Expressed in all major tissues, with higher expression in green parts. Its expression is light-dependent and regulated at the mRNA level. Activates the cysteine desulfurase activity of CpNifS for chloroplastic iron-sulfur cluster biogenesis.	0.99	2.77
At4g35640	ATSERAT3;2 (cytosolic serine O-acetyltransferase, sulfur assimilation and cysteine biosynthesis. Expressed in the vascular system. Expression is induced in both roots and shoots under sulfur-starved conditions.	1.21	2.19
At4g39120	inositol monophosphatase family protein, low similarity to Monophosphatase (Streptomyces anulatus) GI:1045231; contains Pfam profile PF00459: Inositol monophosphatase family	1.18	1.03
At4g39940	AKN2 (adenylylsulfate kinase 2 (AKN2), identical to adenylylsulfate kinase 2, chloroplast precursor (APS kinase, Adenosine-5'-phosphosulfate kinase, ATP adenosine-5'- phosphosulfate 3'-phosphotransferase) (Arabidopsis thaliana) SWISS-PROT:O49196	1.06	1.82
At5g09290	3'(2'),5'-bisphosphate nucleotidase, putative / inositol polyphosphate 1-phosphatase, putative, similar to SP Q42546 3'(2'),5'-bisphosphate	0.88	1.70

	nucleotidase (EC 3.1.3.7) {Arabidopsis thaliana}; contains Pfam profile PF00459: Inositol monophosphatase family		
At5g28020	Bsas4;2 (cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, similar to O-acetylserine(thiol) lyase (EC 4.2.99.8) (Brassica juncea) GI:2245144; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme	1.04	1.97
At5g43780	APS4 (sulfate adenylyltransferase 4 / ATP-sulfurylase 4 (APS4), identical to ATP sulfurylase precursor (APS4) (Arabidopsis thaliana) GI:4633131	1.10	1.59
At5g44720	molybdenum cofactor sulfurase family protein, weak similarity to molybdenum cofactor sulfurase (LOS5/ABA3) (Arabidopsis thaliana) GI:15407262; contains Pfam profiles PF03476: MOSC N-terminal beta barrel domain, PF03473: MOSC domain	1.15	1.74
At5g49940	NFU2 (nitrogen fixation NifU-like family protein, similar to Nitrogen fixation protein nifU (SP:Q43885) {Anabaena azollae}; contains Pfam profile: PF01106 NifU-like domain	1.46	1.64
At5g54390	AHL (inositol monophosphatase family protein, similar to SP Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) {Arabidopsis thaliana}; contains Pfam profile PF00459: Inositol monophosphatase family; supporting cDNA gi 1354509 gb U55205.1 ATU55205	1.13	3.31
At5g55130	CNX5 (molybdenum cofactor synthesis protein 3 / molybdopterin synthase sulphurylase (CNX5), identical to SP Q9ZNW0 Molybdenum cofactor synthesis protein 3 (Molybdopterin synthase sulfurylase) (MPT synthase sulfurylase) {Arabidopsis thaliana}; contains Pfam profiles PF00899: ThiF family, PF00581: Rhodanese-like domain, PF05237: MoeZ/MoeB domain	0.89	2.06
At5g56760	Serat1;1 (serine O-acetyltransferase (SAT-52), cytosol, root vascular system, cotyledon vascular system, serine O-acetyltransferase activity, cysteine biosynthetic process from serine identical to GI:905391	1.06	4.08
At5g63980	SAL1 (3'(2'),5'-bisphosphate nucleotidase / inositol polyphosphate 1-phosphatase / FIERY1 protein (FRY1) (SAL1), identical to SP Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) (3'(2'),5'-bisphosphonucleoside 3'(2')-phosphohydrolase) (DPNPase) {Arabidopsis thaliana}; identical to cDNA inositol polyphosphate 1-phosphatase FIERY1 (FRY1) GI:15281147	1.24	2.11
At5g63990	3'(2'),5'-bisphosphate nucleotidase, putative / inositol polyphosphate 1-phosphatase, putative, similar to SP Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) {Arabidopsis thaliana}; contains Pfam profile PF00459: Inositol monophosphatase family	1.06	2.31
At5g64000	SAL2 (3'(2'),5'-bisphosphate nucleotidase, putative / inositol polyphosphate 1-phosphatase, putative, similar to SP Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) {Arabidopsis thaliana}; contains Pfam profile PF00459: Inositol monophosphatase family	0.84	2.24
At5g65720	AtMtNifS (cysteine desulfurase whose activity is dependent on AtSufE activation)	1.07	1.73
At5g67520	AKN4 (adenylylsulfate kinase, putative, similar to adenylylsulfate kinase, chloroplast precursor (APS kinase, Adenosine-5'-phosphosulfate kinase, ATP adenosine-5'- phosphosulfate 3'-phosphotransferase) (Catharanthus roseus) SWISS-PROT:O49204	0.90	1.76
At1g23090	Sultr3;3 Sulfate Transporter (AST91 mRNA for sulfate transporter) integral to membrane, sulfate transmembrane transporter activity, sulfate transport,	1.07	2.34
At1g77990	Sultr2;2 (similar to sulfate transporter [Arabidopsis thaliana])	0.99	1.66
At3g51895	Sultr3;1 (Arabidopsis thaliana mRNA for sulfate transporter, complete cds.	1.07	1.13
At4g02700	Sultr3;2 (Arabidopsis thaliana mRNA for sulfate transporter)	0.82	1.39

At5g10180	Sultr2;1 (sulfate transporter, Encodes a low-affinity sulfate transporter expressed in the root cap and central cylinder	0.81	1.67
At5g13550	Sultr4;1 (Arabidopsis thaliana mRNA for sulfate transporter, complete cds.)	0.69	1.40
At1g78000	SULTR1;2 (SEL1, SELENATE RESISTANT 1, SULFATE TRANSPORTER)	0.87	1.86
At3g12520	Sultr4;2 Sulfate transporter that is induced under sulfate limitation. (Arabidopsis thaliana mRNA for sulfate transporter, complete cds.) membrane, sulfate transmembrane transporter activity,	0.89	2.00
At3g15990	Sultr3;4 (Arabidopsis thaliana mRNA for sulfate transporter)	0.80	1.80
At5g19600	SULTR3;5 (Arabidopsis thaliana Sultr3;5 mRNA for sulfate transporter, complete cds)	0.69	1.74
At3g45710	POT proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family membrane, transporter activity, oligopeptide transport	0.94	2.20
At3g44860	S-adenosylmethionine-dependent methyltransferase activity, biological process unknown S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to defense-related protein cjs1 (Brassica carinata)(GI:14009292)(Mol Plant Pathol (2001) 2(3):159-169)	1.00	2.06
At2g10940	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to proline-rich cell wall protein (Medicago sativa) GI:3818416; contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family	0.77	1.74
At1g12900	glyceraldehyde 3-phosphate dehydrogenase, glycolysis, chloroplast, putative / NADP-dependent glyceraldehydephosphate dehydrogenase, putative,	2.81	3.11
At3g01120	cystathionine gamma-synthase activity, methionine biosynthetic process, cystathionine gamma-synthase, chloroplast / O-succinylhomoserine (Thiol)-lyase (CGS), identical to SP P55217 Cystathionine gamma-synthase, chloroplast precursor (EC 4.2.99.9) (CGS) (O-succinylhomoserine (Thiol)-lyase) {Arabidopsis thaliana})	1.23	2.32
At3g57050	cystathionine beta-lyase, chloroplast / beta-cystathionase / cysteine lyase (CBL), identical to SP P53780 Cystathionine beta-lyase, chloroplast precursor (EC 4.4.1.8) (CBL) (Beta-cystathionase) (Cysteine lyase) {Arabidopsis thaliana}	1.04	1.32
At4g23100	GSH1 (glutamate-cysteine ligase / gamma-glutamylcysteine synthetase (GSH1), identical to glutamate-cysteine ligase SP:P46309 from (Arabidopsis thaliana)	1.01	1.26
At5g27380	GSH2 (glutathione synthetase (GSH2), non-consensus AT donor splice site at exon 6, AC acceptor splice site at exon 7; identical to Swiss-Prot:P46416 glutathione synthetase, chloroplast precursor (Glutathione synthase) (GSH synthetase) (GSH-S) (Arabidopsis thaliana))	0.87	1.40
At2g15290	potential chloroplast iron transporter	0.94	1.19
At5g44340	Tublin4, beta tubulin gene, structural constituent of cytoskeleton, tubulin complex, leaf	0.74	1.09
At5g19510	Elongation factor 1	1.00	1.30
At2g14610	PR1 Pathogenesis related protein gene expression is induced in response to a variety of pathogens. It is a useful molecular marker for the SAR response	0.73	0.37
At3g57260	PR2 Pathogenesis related protein 2 cellulase activity, systemic acquired resistance	0.77	0.41
At1g75040	PR5 Pathogenesis related protein 5, Thaumatin-like protein involved in response to pathogens.	0.63	0.16
At2g37040	PAL1 phenylalanine ammonia-lyase cytoplasm, defense response, response to oxidative stress, response to wounding, phenylalanine ammonia-lyase activity	1.16	1.30
At3g04720	PR4 Pathogenesis related protein 4, chitin binding, response to virus, systemic acquired resistance, response to ethylene stimulus	0.73	0.31
At5g44420	PDF1.2 Plant defensin 1.2	0.56	0.37

At4g11280	AtACS6 ethylene biosynthetic process, 1-aminocyclopropane-1-carboxylate (ACC) synthase (S-adenosyl-L-methionine methylthioadenosine-lyase, EC 4.4.1.14) gene family	0.45	0.36
At5g24780	AtVSP1 Acid phosphatase, Gene expression is induced by wounding and jasmonate	0.40	0.34
At2g02100	Pin2 protease inhibitor Low-molecular-weight cysteine-rich.	0.24	0.25
At5g42650	AOS Allene oxide synthase enzyme catalyzes dehydration of the hydroperoxide to an unstable allene oxide in the JA biosynthetic pathway.	0.75	1.31
At5g52310	rd29a response to cold, response to water deprivation, response to salt stress, response to abscisic acid stimulus, dry seed stage	0.76	1.30
At1g32640	rd22 Encodes a MYC-related transcriptional activator with a typical DNA binding domain of a basic helix-loop-helix leucine zipper	0.62	0.73
At1g02950	GST3 glutathione transferase, breakdown of toxin, glutathione conjugation reaction; glutathione S-alkyltransferase activity; S-(hydroxyalkyl)glutathione lyase activity; glutathione S-aryltransferase activity; glutathione S-transferase activity; glutathione S-aryltransferase activity; RX:glutathione R-transferase activity; glutathione S-alkyl transferase activity	0.62	0.41
At3g45640	MPK3 mitogen-activated kinase whose mRNA levels increase in response to touch, cold, salinity stress and chitin oligomers.	1.02	0.66
At4g01370	MPK4 mitogen-activated kinase whose mRNA levels increase in response to touch, cold, salinity stress and chitin oligomers.	0.97	0.68
At2g43790	MPK6 mitogen-activated kinase whose mRNA levels increase in response to touch, cold, salinity stress and chitin oligomers.	1.08	0.79

Supplemental Table 2.

Gene set 1	Roots	Fold induction by selenate	
AGI code	Annotation	<i>S. albescens</i>	<i>S. pinnata</i>
At1g67810	CpSufE2 Fe-S metabolism associated domain-containing protein; similar to QS (QUINOLINATE SYNTHASE), quinolinate synthetase A [Arabido....	2.33	0.90
At5g50210	CpSufE3	0.71	0.83
At4g04770	CpSufB	1.13	1.23
At3g10670	CpSufC	0.82	0.97
At1g32500	CpSufD	0.74	0.85
At3g24430	HCF101	0.76	0.78
At1g64810	APO1	0.66	0.79
At1g03850	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	1.34	0.60
At1g32760	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	0.67	0.66
At2g20270	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	1.21	1.51
At2g38270	chloroplastic glutaredoxin electron transport, thiol-disulfide	0.81	1.57

	exchange intermediate activity		
At2g41330	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	0.82	1.14
At3g15660	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	2.09	2.91
At3g54900	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	0.92	1.19
At3g57070	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	0.68	0.96
At4g28730	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	1.19	1.45
At5g11930	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	1.00	0.81
At5g13810	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	0.81	0.86
At5g58530	chloroplastic glutaredoxin electron transport, thiol-disulfide exchange intermediate activity	0.66	0.86
At3g62930	glutaredoxin affected by Se, cellular component unknown, arsenate reductase (glutaredoxin) activity, electron transport, thiol-disulfide exchange intermediate activity	0.78	0.97
At1g28480	glutaredoxin affected by Se, electron transport, jasmonic acid mediated signaling pathway, salicylic acid mediated signaling pathway, thiol-disulfide exchange intermediate activity, response to salicylic acid stimulus	0.78	2.73
At5g04590	SIR (sulfite reductase, plastid, sulfite reductase activity, sulfate reduction	2.24	2.70
At2g15620	nitrite reductase	0.84	2.18
At1g10960	ferredoxin	0.70	0.92
At1g32550	ferredoxin	1.17	1.03
At2g27510	ferredoxin	4.36	2.58
At1g60950	ferredoxin	1.55	1.22
AtCg00350	PsaA/B	0.82	1.88
AtCg01060	PsaC (chloroplast thylakoid membrane, electron carrier activity, iron ion binding	1.34	1.60
At5g04140	glutamate synthase, ferredoxin dependent glutamate synthase (Fd-GOGAT). Expression in leaves is induced by light and sucrose. Proposed to be involved in photorespiration and nitrogen assimilation.	0.69	0.83

At4g03280	Rieske protein involved photosynthetic electron transport cytochrome b6/f, nonphotochemical quenching, encodes the FeS center of cytochrome b6f complex	2.25	0.97
At4g29890	choline monooxygenase	1.17	1.02
At4g34740	Amidophosphoribosyltransferase	0.84	1.41
At3g23940	Dihydroxy-acid dehydratase, branched chain family amino acid biosynthetic process, isoleucine biosynthetic process, metabolic process, valine biosynthetic process dehydratase family; similar to dihydroxy-acid dehydratase [Rhodopirellula baltica SH 1] (GB:NP_870314.1); similar to dihydrox....	1.14	2.35
At2g04700	Ferredoxin-thioredoxin reductase	1.03	1.47
At1g45904	NADH-plastoquinone oxidoreductase	0.41	0.86
AtCg01090	subunit I (NdhI)	0.60	0.86
At3g44880	Pheophorbide a oxygenase (LLS1)	0.93	0.99
At1g50170	Sirohydrochlorin ferrochelataase	0.97	1.12
At2g24820	Tic55, plastid protein import	0.68	1.10
At4g25650	Tic55, plastid protein import	0.69	1.12
At1g03130	PsaD	0.75	1.16
At1g67090	Rubisco SSU	3.21	1.19
At4g34900	xanthine dehydrogenase	1.02	1.08
At2g31955	xanthine dehydrogenase	1.05	1.37
At2g43360	biotin synthase	1.52	1.95
At2g25080	GPX GSH peroxidase chloroplast, glutathione peroxidase activity, response to oxidative stress	1.16	1.21
At2g31570	AtGPX2 GSH peroxidase glutathione peroxidase activity, response to oxidative stress	2.20	0.98
At3g54660	glutathione reductase (GR)	0.44	1.08
At3g03780	methionine synthase cytosolic, involved in methionine regeneration via the activated methyl cycle (or SAM cycle)	2.38	1.62
At5g17920	methionine synthase cytosolic, cobalamin-independent methionine synthase, involved in methionine regeneration via the activated methyl cycle (SAM cycle). The protein undergoes thiolation following treatment with the oxidant tert-butylhydroperoxide.	2.63	1.57
At5g20980	methionine synthase chloroplastic	0.89	1.20

At5g49810	methionine methyl transferase	0.75	1.13
At1g64280	NPR-1	0.83	0.75
At1g56600	GALACTINOL SYNTHASE 2 (similar to galactinol synthase-like protein [Thellun (GB:AAM19710.1); contains InterPro domain Glycosyl transferase, family 8; (InterPro:IPR002495) water stress related protein carbohydrate biosynthetic process transferase activity, transferring hexosyl groups, transferase activity, transferring glycosyl groups	0.73	0.66
At5g43840	HSP TF	0.68	0.85
At1g05680	UDP-glycosyltransferase, transferase activity, transferring hexosyl groups, metabolic process, transferase activity, transferring glycosyl groups, UDP-glucuronosyl/UDP-glucosyl transferase family protein; similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein...	1.56	2.25
At1g02850	glycosyl transferase	0.65	0.90
At4g11650	osmotin	0.40	0.51
At2g29490	GSH transferase, toxin catabolic process located in cytoplasm has glutathione transferase activity	0.80	0.86
At5g12030	HSP 17.6	0.46	0.63
At5g52300	response to water deprivation, response to salt stress, response to abscisic acid stimulus, The promoter region contains two ABA-responsive elements (ABREs) that are required for the dehydration-responsive expression of rd29B as cis-acting elements.	0.44	0.63
At5g13170	nodulin MtN3 family protein; similar to MTN3, senescence protein	0.58	0.94
At1g23730	carbonic anhydrase, carbon utilization, functions in zinc ion binding, has carbonate dehydratase activity	0.79	2.87
At3g01500	carbonic anhydrase chloroplast thylakoid membrane, carbonate dehydratase activity, zinc ion binding, carbon utilization	0.76	0.73
At3g51860	Ca/H antiporter	0.70	0.92
At3g63440	cytokinin oxidase	0.64	0.56
At5g44120	legumin-like protein	0.63	0.82
At5g38710	proline oxidase	0.89	1.09
At4g34410	ERB (ethylene receptor) TF	0.67	1.64
At1g12610	Cold binding factor 1 TF	0.66	1.31
At5g12020	HSP 17.6	0.55	0.33

At4g33720	PR (pathogenesis-related protein, putative; similar to ATPRB1 (Arabidopsis thaliana basic pathogenesis-related protein 1)	0.73	1.41
At2g26150	HSP TF	0.45	0.81
At3g46230	HSP17 involved in response to heat, member of the class I small heat-shock protein (sHSP) family, which accounts for the majority of sHSPs in maturing seeds	0.51	0.69
At1g59860	HSP17	0.62	0.61
At1g53540	HSP 17.6	0.60	0.46
At3g12580	HSP70 cytosol, ATP binding, response to heat, protein folding	0.69	0.68
At4g11280	ACC synthase, ethylene biosynthetic process, induction of apoptosis by oxidative stress, encodes a member of the 1-aminocyclopropane-1-carboxylate (ACC) synthase (S-adenosyl-L-methionine methylthioadenosine-lyase	2.79	1.53
At1g27730	STZ (salt tolerant zinc finger, nucleic acid binding, transcription factor activity, zinc ion binding, response to chitin. Related to Cys2/His2-type zinc-finger proteins found in higher plants. Compensated for a subset of calcineurin deficiency in yeast. Salt tolerance produced by ZAT10 appeared to be partially dependent on ENA1/PMR2, a P-type ATPase required for Li ⁺ and Na ⁺ efflux in yeast. The protein is localized to the nucleus, acts as a transcriptional repressor and is responsive to chitin oligomers.	0.90	1.11
At4g02200	drought induced protein	0.90	0.89
At5g51440	mitochondria HSP	0.86	1.19
At3g08490	Chl a/b binding protein	0.61	0.84
At4g02770	PSI D protein	0.97	0.48
At1g52820	gibberellin oxidase	0.60	1.10
At5g04960	pectinesterase	0.64	0.87
At2g46690	auxin regulated protein	0.77	0.59
At2g34370	putative selenium binding protein(pentatricopeptide (PPR) repeat-containing protein)	0.63	0.84
At4g14040	putative selenium binding protein (56kDa selenium binding protein (SBP56))	1.35	0.80
At4g14030	selenium binding protein (56kDa selenium binding protein (SBP56)) putative function in selenium-binding ; Identical to Putative selenium-binding protein [Arabidopsis Thaliana] (GB:O23264); similar to EDA38 (embryo sac development arrest 38), selenium binding [Arabidopsis thaliana] (TAIR:AT4G14040.1); similar to selenium-binding family protein [Arabidopsis thaliana] (TAIR:AT3G23800.1);	2.99	1.17

	similar to selenium binding protein [Lotus japonicus] (GB:CAC67491.1); similar to putative selenium-binding protein [Thellun (GB:AAM19706.1); similar to selenium binding protein [Medicago sativa] (GB:CAC67501.1); contains InterPro domain Quinoprotein amine dehydrogenase, beta chain-like; (InterPro:IPR011044); contains InterPro domain Selenium-binding protein; (InterPro:IPR008826)		
At3g23800	selenium-binding family protein; similar to EDA38, selenium binding [Arabidopsis thaliana] (TAIR:AT4G14040.1); similar to selenium-binding protein, putative [Arabidopsis thaliana] (TAIR:AT4G14030.1); similar to selenium binding protein [Lotus japonicus] (GB:CAC67491.1); similar to selenium binding protein [Glycine max] (GB:CAC67472.1); similar to selenium binding protein [Medicago sativa] (GB:CAC67501.1); contains InterPro domain Quinoprotein amine dehydrogenase, beta chain-like; (InterPro:IPR011044); contains InterPro domain Selenium-binding protein; (InterPro:IPR008826)	1.63	1.34
At2g03880	putative selenium binding protein, pentatricopeptide (PPR) repeat-containing protein; similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:AT3G24000.1); similar to Os06g0472300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001057622.1); similar to PPR986-12 [Physcomitrella patens] (GB:BAD67155.1); contains InterPro domain Pentatricopeptide repeat; (InterPro:IPR002885); contains InterPro domain Protein prenyltransferase; (InterPro:IPR008940); contains InterPro domain Tetratricopeptide-like helical; (InterPro:IPR011990)	0.61	0.86
At2g25580	putative selenium binding protein	0.72	0.97
At5g40415	putative selenium binding protein	0.66	0.84
At5g48910	putative selenium binding protein	0.75	0.90
At1g05720	selenoprotein family protein, contains Prosite PS00190: Cytochrome c family heme-binding site signature; similar to 15 kDa selenoprotein	1.35	0.91
At3g22740	homocysteine S-methyltransferase 3 (HMT-3), identical to homocysteine S-methyltransferase HMT-3 (Arabidopsis thaliana) GI:9966515; similar to homocysteine S-methyltransferase AtHMT-2 (GI:6685163) (Arabidopsis thaliana); similar to selenocysteine methyltransferase GB:P56707 from (Astragalus bisulcatus)	0.59	0.95
At3g47300	selenoprotein-related, contains weak similarity to selenoprotein W	0.69	0.97
At5g58640	similar to selenoprotein-related [Arabidopsis thaliana] (TAIR:At3g47300.1)	1.80	1.17
At1g01910	similar to anion-transporting ATPase family protein	1.03	0.85

At1g08490	AtCpNifS (cysteine desulfurase, putative, similar to nitrogen fixation protein (nifS))	0.98	1.08
At1g10500	AtCplscA (Involved in chloroplast Fe-S cluster assembly. Located in the chloroplast stroma.)	1.59	1.10
At1g16460	ATRDH2 (encodes a cytoplasmic thiosulfate:cyanide sulfurtransferase, activity of which increased the rhodanese activity of transgenic yeast. Can also act as a mercaptopyruvate sulfurtransferase)	0.74	0.93
At1g18490	Chloroplastic NifS-like protein that can catalyze the conversion of cysteine into alanine and elemental sulfur (S(0)) and of selenocysteine into alanine and elemental Se (Se(0)). Overexpression enhances selenium tolerance and accumulation	1.40	1.19
At1g19920	APS2 (sulfate adenylyltransferase 2 / ATP-sulfurylase 2 (ASA1) (MET3-1) (APS2), identical to ATP sulfurylase)	1.86	0.53
At1g30910	molybdenum cofactor sulfurase family protein, weak similarity to molybdenum cofactor sulfurase (LOS5/ABA3)	1.69	1.00
At1g31190	Involved in sulfur metabolic process, inositol or phosphatidylinositol phosphatase activity, located in chloroplast has 3'(2'),5'-bisphosphate nucleotidase activity, inositol or phosphatidylinositol phosphatase activity, inositol monophosphatase family protein, similar to SP P29218 Myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25) (Inositol monophosphatase)	0.96	0.96
At1g51390	NFU5 (nitrogen fixation NifU-like family protein, similar to HIRA-interacting protein 5 (NIFU FAMILY))	0.89	0.78
At1g55880	pyridoxal-5'-phosphate-dependent enzyme, beta family protein, similar to SP P50867 Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) (Aspergillus nidulans) {Emericella nidulans}; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme	0.56	1.04
At1g55920	Serat2;1 (serine O-acetyltransferase, putative, identical to GI:608677 from (Arabidopsis thaliana))	0.65	1.01
At1g62180	APR2 (5'-adenylylsulfate reductase 2, Second enzyme Involved in sulfate reduction, chloroplast (APR2) (APSR) / adenosine 5'-phosphosulfate 5'-adenylylsulfate (APS) sulfotransferase 2 / 3'-phosphoadenosine-5'-phosphosulfate (PAPS) reductase homolog 43 (PRH-43))	1.83	1.41
At1g70560	alliinase C-terminal domain-containing protein, contains Pfam profiles: PF04864 allinase C-terminal domain, PF04863 alliinase EGF-like domain	1.19	1.08
At1g79230	mercaptopyruvate sulfurtransferase (MST1) (RDH1), identical to mercaptopyruvate sulfurtransferase GI:6009981 and thiosulfate sulfurtransferase GI:5834508 from (Arabidopsis	0.71	1.31

	thaliana) encodes a sulfurtransferase/rhodanese, which belongs to a group of enzymes widely distributed in all three phyla that catalyze the transfer of sulfur from a donor to a thiophilic acceptor substrate. The protein and transcript levels are NOT affected by senescence or exogenous cyanide, suggesting that sulfurtransferases are involved in cyanide detoxification.		
At2g14750	AKN1 (adenylylsulfate kinase 1 (AKN1), identical to adenylylsulfate kinase 1, chloroplast precursor (APS kinase, Adenosine-5'-phosphosulfate kinase, ATP adenosine-5'- phosphosulfate 3'-phosphotransferase) (Arabidopsis thaliana) SWISS-PROT:Q43295	3.40	1.20
At2g16710	IscA-like protein (hesB-like domain-containing protein, similar to IscA (putative iron-sulfur cluster assembly protein) (Azotobacter vinelandii) GI:2271523; contains Pfam profile PF01521: HesB-like domain	0.82	0.81
At2g17640	Serat3;1 (serine O-acetyltransferase, putative (SAT-106), similar to Arabidopsis thaliana serine acetyltransferase GI:905391	2.55	1.33
At2g36260	iron-sulfur cluster assembly complex protein, putative, similar to IscA (putative iron-sulfur cluster assembly protein) (Azotobacter vinelandii) GI:2271523; contains Pfam profile PF01521: HesB-like domain	0.70	0.96
At2g43750	Bsas2;1 (cysteine synthase, chloroplast / O-acetylserine (thiol)-lyase / O-acetylserine sulfhydrylase / cpACS1 (OASB), identical to SP P47999 Cysteine synthase, chloroplast precursor (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) (cpACS1) {Arabidopsis thaliana}; identical to cDNA O-acetylserine lyase (At.OAS.7-4) GI:6983575	2.10	1.61
At3g01020	Encodes a mitochondrial protein similar to E.coli IscU. In bacteria, IscU is a scaffold protein accepting sulfur and iron to build a transient Fe-S cluster, which is subsequently transferred to a target apoprotein.	0.53	0.56
At3g02870	inositol-1(or 4)-monophosphatase, putative / inositol monophosphatase, putative / IMPase, putative, similar to SP P54928 Inositol-1(or 4)-monophosphatase 3 (EC 3.1.3.25) (IMPase 3) (IMP 3) (Inositol monophosphatase 3) {Lycopersicon esculentum}; contains Pfam profile PF00459: Inositol monophosphatase family	0.84	0.71
At3g03630	Bsas5;1 (cysteine synthase, chloroplast, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, identical to SP O22682 Probable cysteine synthase, chloroplast precursor {Arabidopsis thaliana}, similar to SP P31300 Cysteine synthase, chloroplast precursor {Capsicum annum}	0.69	0.77

At3g04940	Bsas4;1 (cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, similar to O-acetylserine(thiol) lyase (EC 4.2.99.8) (Brassica juncea) GI:2245144; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme	0.89	1.32
At3g13110	Serat2;2 (serine O-acetyltransferase (SAT-1), identical to serine acetyltransferase (Sat-1) GI:1184048 (Arabidopsis thaliana)	1.08	0.59
At3g20970	NFU4 (nitrogen fixation NifU-like family protein, similar to HIRA-interacting protein 5 (NIFU FAMILY) (SP:Q9QZ23) {Mus musculus}); contains Pfam profile: PF01106 NifU-like domain	1.44	1.05
At3g22460	Bsas1;4 (Cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, nearly identical over 185 amino acids to SP P47998 Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) {Arabidopsis thaliana}	3.58	1.66
At3g22890	APS1 (ATP sulfurylase, the first enzyme in the sulfate assimilation pathway of Arabidopsis)	4.07	1.43
At3g59760	Bsas2;2 (cysteine synthase, mitochondrial, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, similar to SP Q43725 Cysteine synthase, mitochondrial precursor (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) {Arabidopsis thaliana}	2.42	1.65
At3g61440	Bsas3;1 (encodes a cysteine synthase isomer. The isomer is however less effective in cysteine biosynthesis. It is involved in beta-cyanoalanine biosynthesis, a intermediate of cyanide detoxification pathway.	4.27	1.84
At4g01940	NFU1 (nitrogen fixation NifU-like family protein, similar to apricot NifU homolog partial CDS, GenBank accession number U95179; contains Pfam profile: PF01106 NifU-like domain)	1.16	0.97
At4g04080	Encodes a mitochondrial protein similar to E.coli IscU. In bacteria, IscU is a scaffold protein accepting sulfur and iron to build a transient Fe-S cluster, which is subsequently transferred to a target apoprotein.	1.61	0.92
At4g04610	APR1 (5'-adenylylsulfate reductase (APR1) / PAPS reductase homolog (PRH19), identical to 5'-adenylylsulfate reductase (Arabidopsis thaliana) GI:2738756; identical to cDNA PAPS reductase homolog (PRH19) GI:1710111	6.74	1.18
At4g14880	Bsas1;1 (cysteine synthase / O-acetylserine (thiol)-lyase / O-acetylserine sulfhydrylase (OAS1), nearly identical to SP P47998 Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) {Arabidopsis thaliana}; identical to cDNA O-acetylserine lyase	2.22	1.28

	(At.OAS.5-8) GI:6983573		
At4g21990	APR3 (5'-adenylylsulfate reductase (APR3) Second enzyme Involved in sulfate reduction/ PAPS reductase homolog (PRH26), identical to 5'-adenylylsulfate reductase (Arabidopsis thaliana) GI:2738760; identical to cDNA PAPS reductase homolog (PRH26) GI:1710113	4.36	2.03
At4g22220	ISU1 (iron-sulfur cluster assembly complex protein, putative, similar to iron-sulfur cluster assembly complex ISCU1 (GI:11545705) (Homo sapiens); nifU protein homolog YPL135w (GI:15619823) (Saccharomyces cerevisiae) PIR2:S69049)	1.08	1.30
At4g24670	Allinase family protein, Carbon-sulfur lyase activity, endomembrane system, contains Pfam profiles: PF04864 allinase C-terminal domain, PF04863 alliinase EGF-like domain	0.81	0.89
At4g25910	NFU3 (nitrogen fixation protein, putative, nitrogen fixation protein nifU (SP:Q43885) (Anabaena sp.); contains Pfam profile: PF01106 NifU-like domain)	0.70	0.79
At4g26500	AtSufE (Sulfur acceptor that interacts with and activates the cysteine desulfurases, AtSufS in plastids and AtNifS1 in mitochondria, and both activations are vital during embryogenesis. Dual localization in mitochondria and chloroplasts. Involved in Fe-S cluster biogenesis in mitochondria and plastids. Expressed in all major tissues, with higher expression in green parts. Its expression is light-dependent and regulated at the mRNA level. Activates the cysteine desulfurase activity of CpNifS for chloroplastic iron-sulfur cluster biogenesis.	0.84	1.07
At4g35640	ATSERAT3;2 (cytosolic serine O-acetyltransferase, sulfur assimilation and cysteine biosynthesis. Expressed in the vascular system. Expression is induced in both roots and shoots under sulfur-starved conditions.	0.93	1.06
At4g39120	inositol monophosphatase family protein, low similarity to Mono-phosphatase (Streptomyces anulatus) GI:1045231; contains Pfam profile PF00459: Inositol monophosphatase family	0.49	0.94
At4g39940	AKN2 (adenylylsulfate kinase 2 (AKN2), identical to adenylylsulfate kinase 2, chloroplast precursor (APS kinase, Adenosine-5'-phosphosulfate kinase, ATP adenosine-5'- phosphosulfate 3'-phosphotransferase) (Arabidopsis thaliana) SWISS-PROT:O49196	3.16	1.38
At5g09290	3'(2'),5'-bisphosphate nucleotidase, putative / inositol polyphosphate 1-phosphatase, putative, similar to SP Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) {Arabidopsis thaliana}; contains Pfam profile PF00459: Inositol monophosphatase family	1.07	1.03
At5g28020	Bsas4;2 (cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase,	3.42	1.56

	putative, similar to O-acetylserine(thiol) lyase (EC 4.2.99.8) (Brassica juncea) GI:2245144; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme		
At5g43780	APS4 (sulfate adenyltransferase 4 / ATP-sulfurylase 4 (APS4), identical to ATP sulfurylase precursor (APS4) (Arabidopsis thaliana) GI:4633131	0.79	0.96
At5g44720	molybdenum cofactor sulfurylase family protein, weak similarity to molybdenum cofactor sulfurylase (LOS5/ABA3) (Arabidopsis thaliana) GI:15407262; contains Pfam profiles PF03476: MOSC N-terminal beta barrel domain, PF03473: MOSC domain	1.57	0.98
At5g49940	NFU2 (nitrogen fixation NifU-like family protein, similar to Nitrogen fixation protein nifU (SP:Q43885) {Anabaena azollae}; contains Pfam profile: PF01106 NifU-like domain	1.08	1.53
At5g54390	AHL (inositol monophosphatase family protein, similar to SP Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) {Arabidopsis thaliana}; contains Pfam profile PF00459: Inositol monophosphatase family; supporting cDNA gi 1354509 gb U55205.1 ATU55205	0.69	1.30
At5g55130	CNX5 (molybdenum cofactor synthesis protein 3 / molybdopterin synthase sulphurylase (CNX5), identical to SP Q9ZNW0 Molybdenum cofactor synthesis protein 3 (Molybdopterin synthase sulfurylase) (MPT synthase sulfurylase) {Arabidopsis thaliana}; contains Pfam profiles PF00899: ThiF family, PF00581: Rhodanese-like domain, PF05237: MoeZ/MoeB domain	0.80	0.91
At5g56760	Serat1;1 (serine O-acetyltransferase (SAT-52), cytosol, root vascular system, cotyledon vascular system, serine O-acetyltransferase activity, cysteine biosynthetic process from serine identical to GI:905391	0.70	0.62
At5g63980	SAL1 (3'(2'),5'-bisphosphate nucleotidase / inositol polyphosphate 1-phosphatase / FIERY1 protein (FRY1) (SAL1), identical to SP Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) (3'(2'),5- bisphosphonucleoside 3'(2')-phosphohydrolase) (DPNPase) {Arabidopsis thaliana}; identical to cDNA inositol polyphosphate 1-phosphatase FIERY1 (FRY1) GI:15281147	3.43	2.07
At5g63990	3'(2'),5'-bisphosphate nucleotidase, putative / inositol polyphosphate 1-phosphatase, putative, similar to SP Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) {Arabidopsis thaliana}; contains Pfam profile PF00459: Inositol monophosphatase family	1.89	1.14
At5g64000	SAL2 (3'(2'),5'-bisphosphate nucleotidase, putative / inositol polyphosphate 1-phosphatase, putative, similar to SP Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) {Arabidopsis thaliana}; contains Pfam profile PF00459: Inositol monophosphatase family	2.33	1.26

At5g65720	AtMtNifS (cysteine desulfurase whose activity is dependent on AtSufE activation)	2.59	1.29
At5g67520	AKN4 (adenylylsulfate kinase, putative, similar to adenylylsulfate kinase, chloroplast precursor (APS kinase, Adenosine-5'-phosphosulfate kinase, ATP adenosine-5'-phosphosulfate 3'-phosphotransferase) (Catharanthus roseus) SWISS-PROT:O49204	1.17	1.11
At1g23090	Sultr3;3 Sulfate Transporter (AST91 mRNA for sulfate transporter) integral to membrane, sulfate transmembrane transporter activity, sulfate transport,	0.62	1.31
At1g77990	Sultr2;2 (similar to sulfate transporter [Arabidopsis thaliana])	0.91	1.16
At3g51895	Sultr3;1 (Arabidopsis thaliana mRNA for sulfate transporter, complete cds.	0.69	0.93
At4g02700	Sultr3;2 (Arabidopsis thaliana mRNA for sulfate transporter)	0.61	0.49
At5g10180	Sultr2;1 (sulfate transporter, Encodes a low-affinity sulfate transporter expressed in the root cap and central cylinder	0.82	0.85
At5g13550	Sultr4;1 (Arabidopsis thaliana mRNA for sulfate transporter, complete cds.)	1.30	0.88
At1g78000	SULTR1;2 (SEL1, SELENATE RESISTANT 1, SULFATE TRANSPORTER)	2.55	1.36
At3g12520	Sultr4;2 Sulfate transporter that in induced under sulfate limitation. (Arabidopsis thaliana mRNA for sulfate transporter, complete cds.) membrane, sulfate transmembrane transporter activity,	0.79	1.08
At3g15990	Sultr3;4 (Arabidopsis thaliana mRNA for sulfate transporter)	0.73	1.26
At5g19600	SULTR3;5 (Arabidopsis thaliana Sultr3;5 mRNA for sulfate transporter, complete cds)	0.62	0.84
At3g45710	POT proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family membrane, transporter activity, oligopeptide transport	0.65	1.03
At3g44860	S-adenosylmethionine-dependent methyltransferase activity, biological process unknown S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to defense-related protein cjs1 (Brassica carinata)(GI:14009292)(Mol Plant Pathol (2001) 2(3):159-169)	0.77	0.90
At2g10940	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to proline-rich cell wall protein (Medicago sativa) GI:3818416; contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family	0.81	1.22
At1g12900	glyceraldehyde 3-phosphate dehydrogenase, glycolysis, chloroplast, putative / NADP-dependent	0.78	1.29

	glyceraldehydephosphate dehydrogenase, putative,		
At3g01120	cystathionine gamma-synthase activity, methionine biosynthetic process, cystathionine gamma-synthase, chloroplast / O-succinylhomoserine (Thiol)-lyase (CGS), identical to SP P55217 Cystathionine gamma-synthase, chloroplast precursor (EC 4.2.99.9) (CGS) (O-succinylhomoserine (Thiol)-lyase) {Arabidopsis thaliana}	2.27	2.24
At3g57050	cystathionine beta-lyase, chloroplast / beta-cystathionase / cysteine lyase (CBL), identical to SP P53780 Cystathionine beta-lyase, chloroplast precursor (EC 4.4.1.8) (CBL) (Beta-cystathionase) (Cysteine lyase) {Arabidopsis thaliana}	1.20	1.47
At4g23100	GSH1 (glutamate-cysteine ligase / gamma-glutamylcysteine synthetase (GSH1), identical to glutamate-cysteine ligase SP:P46309 from (Arabidopsis thaliana)	2.62	1.92
At5g27380	GSH2 (glutathione synthetase (GSH2), non-consensus AT donor splice site at exon 6, AC acceptor splice site at exon 7; identical to Swiss-Prot:P46416 glutathione synthetase, chloroplast precursor (Glutathione synthase) (GSH synthetase) (GSH-S) (Arabidopsis thaliana))	1.67	0.99
At2g15290	potential chloroplast iron transporter	1.37	1.13
At5g44340	Tublin4, beta tubulin gene, structural constituent of cytoskeleton, tubulin complex, leaf	6.33	3.10
At5g19510	Elongaton factor 1	1.00	1.18
At2g14610	PR1 Pathogenesis related protein gene expression is induced in response to a variety of pathogens. It is a useful molecular marker for the SAR response	1.15	0.63
At3g57260	PR2 Pathogenesis related protein 2 cellulase activity, systemic acquired resistance	0.69	0.64
At1g75040	PR5 Pathogenesis related protein 5, Thaumatin-like protein involved in response to pathogens.	1.02	0.34
At2g37040	PAL1 phenylalanine ammonia-lyase cytoplasm, defense response, response to oxidative stress, response to wounding, phenylalanine ammonia-lyase activity	0.73	0.90
At3g04720	PR4 Pathogenesis related protein 4, chitin binding, response to virus, systemic acquired resistance, response to ethylene stimulus	0.87	0.98
At5g44420	PDF1.2 Plant defensin 1.2	0.33	0.60
At4g11280	AtACS6 ethylene biosynthetic process, 1-aminocyclopropane-1-carboxylate (ACC) synthase (S-adenosyl-L-methionine methylthioadenosine-lyase, EC 4.4.1.14) gene family	0.89	1.09

At5g24780	AtVSP1 Acid phosphatase, Gene expression is induced by wounding and jasmonate	1.03	0.60
At2g02100	Pin2 protease inhibitor Low-molecular-weight cysteine-rich.	1.62	0.77
At5g42650	AOS Allene oxide synthase enzyme catalyzes dehydration of the hydroperoxide to an unstable allene oxide in the JA biosynthetic pathway.	0.57	1.07
At5g52310	rd29a response to cold, response to water deprivation, response to salt stress, response to abscisic acid stimulus, dry seed stage	1.01	0.59
At1g32640	rd22 Encodes a MYC-related transcriptional activator with a typical DNA binding domain of a basic helix-loop-helix leucine zipper	0.63	0.73
At1g02950	GST3 glutathione transferase, breakdown of toxin, glutathione conjugation reaction; glutathione S-alkyltransferase activity; S-(hydroxyalkyl)glutathione lyase activity; glutathione S-aralkyltransferase activity; glutathione S-transferase activity; glutathione S-aryltransferase activity; RX:glutathione R-transferase activity; glutathione S-alkyl transferase activity	0.64	0.73
At3g45640	MPK3 mitogen-activated kinase whose mRNA levels increase in response to touch, cold, salinity stress and chitin oligomers.	0.61	0.90
At4g01370	MPK4 mitogen-activated kinase whose mRNA levels increase in response to touch, cold, salinity stress and chitin oligomers.	0.57	1.01
At2g43790	MPK6 mitogen-activated kinase whose mRNA levels increase in response to touch, cold, salinity stress and chitin oligomers.	0.60	0.96

Supplemental Table 3.

Gene set 2	Shoots	Fold induction by selenate	
AGI code	Annotation	<i>S. albens</i>	<i>S. pinnata</i>
At1g74710	ICS1 (isochorismate synthase 1 / isochorismate mutase, identical to GI:17223087 and GB:AF078080; contains Pfam profile PF00425: chorismate binding enzyme; contains TIGRfam profile TIGR00543: isochorismate synthases; identical to cDNA isochorismate synthase 1 precursor (ICS1) nuclear gene for plastid product GI:17223086	0.80	1.52
At3g53260	PAL2 (phenylalanine ammonia-lyase 2 , nearly identical to SP P45724	1.23	1.31
At3g48090	EDS1 (disease resistance protein, identical to disease resistance protein/lipase homolog EDS1 GI:4454567; contains Pfam profile PF01764: Lipase	1.10	1.28
At4g39030	EDS5 (enhanced disease susceptibility 5 / salicylic acid induction deficient 1 (SID1), identical to SP Q945F0; contains Pfam profile PF01554: Uncharacterized membrane protein family	1.08	1.06

At3g52430	PAD4 (Encodes a lipase-like gene that is important for salicylic acid signaling and function in resistance (R) gene-mediated and basal plant disease resistance. PAD4 can interact directly with EDS1, another disease resistance signaling protein. Expressed at elevated level in response to green peach aphid (GPA) feeding, and modulates the GPA feeding-induced leaf senescence through a mechanism that doesn't require camalexin synthesis and salicylic acid (SA) signaling.	1.08	1.77
At5g64930	CPR5 (Constitutive expressor of Pathogenesis Related genes 5 (cpr5); regulator of disease resistance and senescence (Plant J. (2001)26(4)409-420.	0.92	1.49
At1g64280	NPR1 (This gene is a key regulator of the salicylic acid (SA)-mediated systemic acquired resistance (SAR) pathway. It is similar to the transcription factor inhibitor I kappa B, and contains ankyrin repeats. It confers resistance to the pathogens Pseudomonas syringae and Peronospora parasitica in a dosage-dependent fashion. Although transgenic Arabidopsis plants overexpressing NPR1 acquire enhanced sensitivity to SA and (benzothiadiazole) BTH, they display no obvious detrimental morphological changes and do not have elevated pathogenesis-related gene expression until activated by inducers or pathogens	1.04	2.04
At2g14610	PR1 (gene expression is induced in response to a variety of pathogens. It is a useful molecular marker for the SAR response. Though the Genbank record for the cDNA associated to this gene is called 'PR-1-like', the sequence actually corresponds to PR1. Expression of this gene is salicylic-acid responsive	1.32	0.82
At1g75040	PR5 (Thaumatin-like protein involved in response to pathogens. mRNA level of the PR-5 gene (At1g75040) is significantly changed after cutting the inflorescence stem indicating the existence of a network of signal transducing pathways as other stress-regulated genes (At5g01410, At3g17800, At1g29930) do not response to the treatment.	1.29	0.51
At1g02930	GST1 (glutathione S-transferase, putative, similar to glutathione S-transferase Gl:860955 from (Hyoscyamus muticus)	0.89	1.54
At3g57260	PR2a (glycosyl hydrolase family 17 protein, similar to glucan endo-1,3-beta-glucosidase, acidic isoform precursor SP:P33157 from (Arabidopsis thaliana)	1.08	0.70
At1g75800	PR5K (similar to receptor serine/threonine kinase.	1.08	0.46
At1g02860	BAH1(benzoic acid hypersensitive1.	0.84	1.24
At1g02450	NIMIN1 (modulates PR gene expression according the following model: NPR1 forms a ternary complex with NIMIN1 and TGA factors upon SAR induction that binds to a positive regulatory cis-element of the PR-1 promoter, termed LS7. This leads to PR-1 gene induction. NIMIN1 decreases transcriptional activation, possibly through its EAR motif, which results in fine-tuning of PR-1 gene expression.	1.18	1.57
At1g29690	CAD1 (Encodes a protein containing a domain with significant homology to the MACPF (membrane attack complex and perforin) domain of complements and perforin proteins that are involved in innate immunity in	0.99	1.02

	animals. Transgenic cad1-1 mutant plants show lesions seen in the hypersensitive response, as well as a spontaneous activation of expression of pathogenesis-related genes and leading to a 32-fold increase in salicylic acid (SA). CAD1 is postulated to act as a negative regulator controlling SA-mediated pathway of programmed cell death in plant immunity.		
At3g56400	WRKY70 (family transcription factor, DNA-binding protein 4 WRKY4 - Nicotiana tabacum, EMBL:AF193771	1.00	0.99
At4g11280	ACS6 (encodes a a member of the 1-aminocyclopropane-1-carboxylate (ACC) synthase (S-adenosyl-L-methionine methylthioadenosine-lyase, EC 4.4.1.14) gene family	1.31	1.09
At3g04720	PR4 (Encodes a protein similar to the antifungal chitin-binding protein hevein from rubber tree latex. mRNA levels increase in response to ethylene and turnip crinkle virus infection.	0.97	1.15
At1g66340	ETR1 (ethylene receptor 1 , identical to GB:P49333 from (Arabidopsis thaliana) (Science 262 (5133), 539-544 (1993))	1.00	1.22
At3g20770	EIN3 (ethylene-insensitive 3, identical to ethylene-insensitive3 GI:2224933 from (Arabidopsis thaliana)	1.05	1.31
At5g03730	CTR1 (Homologous to the RAF family of serine/threonine protein kinases. Negative regulator in the ethylene signal transduction pathway. Interacts with the putative ethylene receptors ETR1 and ERS. Constitutively expressed.	1.04	1.11
At5g44420	PDF1.2 (Encodes an ethylene- and jasmonate-responsive plant defensin. mRNA levels are not responsive to salicylic acid treatment	0.97	0.52
At3g12500	PR3 (encodes a basic chitinase involved in ethylene/jasmonic acid mediated signalling pathway during systemic acquired resistance based on expression analyses.	1.20	0.63
At4g02520	GSTF2 (Encodes glutathione transferase belonging to the phi class of GSTs. Naming convention according to Wagner et al. (2002). The expression of this gene is upregulated by herbicide safeners such as benoxacor and fenclorim.	1.15	0.74
At1g02500	SAM1 (S-adenosylmethionine synthetase. SAM1 is regulated by protein S-nitrosylation. The covalent binding of nitric oxide (NO) to the Cys114 residue inhibits the enzyme activity.	1.87	2.27
At4g01850	SAM2 (S-adenosylmethionine synthetase 2, identical to S-adenosylmethionine synthetase 2 (Methionine adenosyltransferase 2, AdoMet synthetase 2) (Arabidopsis thaliana) SWISS-PROT:P17562	0.76	1.03
At1g05010	EAT1 (1-aminocyclopropane-1-carboxylate oxidase / ACC oxidase / ethylene-forming enzyme (ACO) (EAT1), Identical to 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) gb X66719 (EAT1). ESTs gb T43073, gb T5714, gb R90435, gb R44023, gb AA597926, gb AI099676, gb AA650810 and gb 29725 come from this gene	0.89	1.29
At1g62380	ACO2 (1-aminocyclopropane-1-carboxylic oxidase (ACC oxidase). Expression of the AtACO2 transcripts is affected by ethylene.	0.89	0.80

At2g40940	ERS1 (Ethylene receptor, subfamily 1. Has histidine kinase activity.	1.14	0.99
At4g20880	ERT2 (ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2), identical to ethylene-regulated nuclear protein (Arabidopsis thaliana) gi 2765442 emb CAA75349	1.08	1.04
At3g16770	EBP(RAP2.3) Encodes a member of the ERF (ethylene response factor) subfamily B-2 of the plant specific ERF/AP2 transcription factor family (RAP2.3). The protein contains one AP2 domain. There are 5 members in this subfamily including RAP2.2 AND RAP2.12. It is localized to the nucleus and acts as a transcriptional activator through the GCC-box. It has been identified as a suppressor of Bax-induced cell death by functional screening in yeast and can also suppress Bax-induced cell death in tobacco plants. Overexpression of this gene in tobacco BY-2 cells confers resistance to H2O2 and heat stresses. Overexpression in Arabidopsis causes upregulation of PDF1.2 and GST6. It is part of the ethylene signaling pathway and is predicted to act downstream of EIN2 and CTR1, but not under EIN3.	1.16	1.07
At5g61600	EREBP-1 (encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.	1.26	1.45
At3g23240	ERF1 (encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family (ERF1). The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5. EREBP like protein that binds GCC box of ethylene regulated promoters such as basic chitinases. Constitutive expression of ERF1 phenocopies ethylene over production. Involved in ethylene signaling cascade, downstream of EIN2 and EIN3.	0.97	1.31
At2g31230	ERF3 (encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.	1.04	0.90
At5g24780	VSP1 (vegetative storage protein 1, identical to SP O49195 Vegetative storage protein 1 precursor {Arabidopsis thaliana}; contains Pfam profile PF03767: HAD superfamily (subfamily IIIB) phosphatase	1.07	0.56
At2g02100	Pin2 (plant defensin-fusion protein, putative (PDF2.2), plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to SWISS-PROT:O65740	1.06	0.74
At1g55020	LOX1 (JA biosynthesis, lipoxygenase, a defense gene conferring resistance Xanthomonas campestris	1.10	1.16
At3g45140	LOX2 (JA biosynthesis, chloroplast lipoxygenase required for wound-induced jasmonic acid accumulation in Arabidopsis. Mutants are resistant to Staphylococcus aureus and accumulate salicylic acid upon infection.	1.07	1.13
At5g42650	AOS (Allene oxide synthase JA biosynthesis cytochrome p450 CYP74 gene family that functions as an allene oxide synthase. This enzyme catalyzes dehydration of the hydroperoxide to an unstable allene oxide in the	0.73	0.98

	JA biosynthetic pathway		
At3g16470	JIP (JR) JA-responsive gene	0.77	0.80
At5g52310	rd29 (low-temperature-responsive protein 78 (LT178) / desiccation-responsive protein 29A (RD29A)	0.96	0.97
At5g25610	rd22 (dehydration-responsive protein (RD22), identical to SP Q08298 Dehydration-responsive protein RD22 precursor {Arabidopsis thaliana}	1.23	0.90
At5g15970	KIN2 (stress-responsive protein / stress-induced protein (KIN2) / cold-responsive protein (COR6.6) / cold-regulated protein (COR6.6), identical to SP P31169 Stress-induced KIN2 protein (Cold-induced COR6.6 protein) {Arabidopsis thaliana}	1.03	0.96
At1g20440	cor47 (cold regulated gene, amino acid sequence homology with Group II LEA (late embryogenesis abundant) proteins. Also responds to osmotic stress, ABA, dehydration and inhibits e.coli growth while overexpressed.	0.92	1.40
At5g66400	RAB18 (ABA- and drought-induced glycine-rice dehydrin protein The ABA-induced expression of RAB18 was reduced following ACC application, indicating that ethylene inhibits the ABA signaling pathway. RAB18 is also expressed in response to the formation of the phospholipid diacylglycerol pyrophosphate.	0.90	1.14
At2g47730	GSTF8 (Encodes glutathione transferase belonging to the phi class of GSTs. Naming convention according to Wagner et al. (2002).	1.07	1.28
At2g37040	PAL1 (phenylalanine ammonia-lyase	1.79	0.77
At1g51680	4-CL (CoA ligase, which is involved in the last step of the general phenylpropanoid pathway. In addition to 4-coumarate, it also converts ferulate	1.29	1.04
At5g13930	CHS (biosynthesis pathway of all flavonoids	1.37	1.11
At3g24170	GR1 (glutathione reductase, chloroplast [Arabidopsis thaliana] (TAIR:At3g54660.1); similar to glutathione reductase [Mesembryanthemum crystallinum] (GB:CAC13956.1); similar to glutathione-disulfide reductase (EC 1.8.1.7) - turnip (GB:T14394); similar to glutathione reductase [Pisum sativum] (GB:CAA66924.1); similar to Glutathione Reductase precursor [Spinacia oleracea] (GB:BAA07108.1); similar to glutathione reductase [Brassica oleracea] (GB:BAD14936.1); contains InterPro domain Pyridine nucleotide-disulphide oxidoreductase dimerisation domain (InterPro:IPR004099); contains InterPro domain Glutathione reductase, plant (InterPro:IPR006324); contains InterPro domain Mercuric reductase (InterPro:IPR000815); contains InterPro domain Pyridine nucleotide-disulphide oxidoreductase, class I (InterPro:IPR001100); contains InterPro domain FAD-dependent pyridine nucleotide-disulphide oxidoreductase (InterPro:IPR001327); contains InterPro domain Trypanothione reductase (InterPro:IPR001864); contains InterPro domain Pyridine nucleotide-disulphide oxidoreductase, class-II (InterPro:IPR000103)	1.14	1.19
At3g54660	GR2 (glutathione reductase that is most likely localized in the chloroplast.	0.87	1.07
At2g25080	GPX1phospholipid hydroperoxide glutathione peroxidase, chloroplast /	0.74	1.03

	PHGPx (GPX1), identical to SP P52032 Phospholipid hydroperoxide glutathione peroxidase, chloroplast precursor (EC 1.11.1.9) (PHGPx) {Arabidopsis thaliana}; contains Glutathione peroxidases signatures, Glutathione_Peroxid_1 (GKVMLIVNVASRCGLT), Glutathione_Peroxid_2 (LAFPCNQF); contains EST GB:T43669, N38679, R30227, H37043, AA042773; identical to cDNA chloroplast mRNA for glutathione peroxidase GI:2274856		
At2g31570	GPX2glutathione peroxidase GPx, cytosolic	1.07	0.87
At1g63460	GPX3glutathione peroxidase, putative, contains Pfam profile: PF00255 glutathione peroxidases	1.02	0.94
At2g43350	GPX4glutathione peroxidase, putative	1.08	1.09
At2g48150	GPX5glutathione peroxidase, putative	0.89	1.24
At3g63080	GPX6glutathione peroxidase, putative, phospholipid-hydroperoxide glutathione peroxidase, spinach, PIR:JC5619	0.92	1.03
At4g11600	GPX7glutathione peroxidase, putative	1.03	1.03
At1g07890	APX1Encodes a cytosolic ascorbate peroxidase. Ascorbate peroxidases scavenge hydrogen peroxide in the cytosol and chloroplasts of plants. At least part of the induction of heat shock proteins during light stress in Arabidopsis is mediated by H2O2 that is scavenged by APX1.	1.28	1.06
At3g09640	APX2cytosol, L-ascorbate peroxidase activity, leaf	1.10	1.26
At4g35000	APX3Encodes a putative peroxisomal ascorbate peroxidase that scavenges H2O2 into peroxisomes and prevents oxidative damage. The protein interacts with AKR2 (ankyrin-containing protein that interacts with AFT1) and AFT1, a 14-3-3 protein.	1.46	0.88
At1g77490	APX4L-ascorbate peroxidase, thylakoid-bound (tAPX), identical to thylakoid-bound ascorbate peroxidase GB:CAA67426 (Arabidopsis thaliana)	1.40	1.15
At4g08390	APX5L-ascorbate peroxidase, stromal (sAPX), identical to stromal ascorbate peroxidase (Arabidopsis thaliana) gi 1419388 emb CAA67425	1.36	1.38
At1g20630	CAT1Catalyzes the reduction of hydrogen peroxide using heme group as cofactor. Protects cells from toxicity by H2O2.	0.77	1.46
At4g35090	CAT2Encodes a peroxisomal catalase, highly expressed in bolts and leaves. mRNA expression patterns show circadian regulation with mRNA levels being high in the subjective early morning.	1.04	1.07
At1g20620	CAT3Catalase, catalyzes the breakdown of hydrogen peroxide (H2O2) into water and oxygen.	0.75	0.71
At1g08830	CSD1copper, zinc superoxide dismutase, cytosolic	1.02	0.88
At2g28190	CSD2 (Chloroplastic	0.99	1.29
At5g18100	CSD3 (Peroxisomal CuZnSOD inducible by a high-light pulse.	0.86	1.16
At4g25100	FSD1 (Superoxide dismutase (Fe), chloroplast (SODB) / iron superoxide dismutase (FSD1), identical to Fe-superoxide dismutase (Arabidopsis	1.05	1.01

	thaliana)		
At5g51100	FSD2 (Superoxide dismutase (Fe), chloroplast (SODB) / iron superoxide dismutase (FSD1), identical to Fe-superoxide dismutase (Arabidopsis thaliana) gi 166700 gb AAA32791; supported by cDNA, Ceres:32935	0.97	1.04
At1g63940	MDAR1 (monodehydroascorbate reductase, putative, similar to monodehydroascorbate reductase GB:AAD28178 (Brassica juncea)	1.22	1.46
At5g03630	MDAR2 (monodehydroascorbate reductase, putative, monodehydroascorbate reductase (NADH), cucumber, PIR:JU0182	2.07	1.19
At3g10920	MSD1 (mitochondrial, superoxide dismutase (Mn), putative / manganese superoxide dismutase, putative [Arabidopsis thaliana] (TAIR:At3g56350.1); similar to superoxide dismutase [Raphanus sativus] (GB:AAL07333.1); contains InterPro domain Manganese and iron superoxide dismutase (InterPro:IPR001189)	2.15	1.26
At3g49120	PRXC (Class III Peroxidase Perx34. Expressed in roots, leaves and stems. Located in the cell wall. Involved in cell elongation. Expression activated by light	1.16	1.40
At2g37130	ATP2a (P96, Peroxidase, peroxidase 21 (PER21) (P21) (PRXR5), identical to SP Q42580 Peroxidase 21 precursor (EC 1.11.1.7) (Atperox P21) (PRXR5) (ATP2a/ATP2b) {Arabidopsis thaliana	0.84	1.32
At3g09390	AtMt1 (Metallothionein, binds to and detoxifies excess copper and other metals, limiting oxidative damage	0.80	0.67
At2g02120	P III (Plant Defensin-fusion protein, putative (PDF2.1), plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); contains a gamma-thionin family signature (PDOC00725)	0.56	0.87
At4g02610	TRPA (tryptophan synthase, alpha subunit, putative, similar to A. thaliana tryptophan synthase alpha chain (EC 4.2.1.20), GenBank accession number U18993 (gi:619753)	1.03	0.97
At5g54810	TRBP (tryptophan synthase, beta subunit 1 (TSB1), identical to SP P14671	1.17	1.00
At5g39580	ATP24a (peroxidase, putative, identical to peroxidase ATP24a (Arabidopsis thaliana) gi 1890313 emb CAA72484 peroxidase activity, response to oxidative stress, N-terminal protein myristoylation, endomembrane system	0.88	1.17
At3g16530	LECT (Lectin like protein whose expression is induced upon treatment with chitin oligomers.	0.82	1.02
At4g39980	DHS1 (2-dehydro-3-deoxyphosphoheptonate aldolase	1.02	1.12
At4g23100	GSH1 (encodes the first enzyme of glutathione (GSH) biosynthesis, gamma-glutamylcysteine synthetase. Required for cell proliferation at the root tip.	1.16	1.37
At5g27380	GSH2 (glutathione synthetase (GSH2), Encodes a protein with similarity to glutathione synthetases, which catalyzes one of the early steps in glutathione biosynthesis. Two transcripts have been detected; the longer transcript is less abundant and the protein is localized to the chloroplast. The smaller transcript, in which the transit peptide is truncated, is localized to the	1.62	1.16

	cytosol.		
At1g19570	mtDHAR (dehydroascorbate reductase mitochondrion, glutathione dehydrogenase (ascorbate) activity, response to jasmonic acid stimulus, response to ozone	2.20	0.90
At1g75270	cytDHAR (dehydroascorbate reductase cytosol	1.10	1.33
At5g16705	DHAR5 (dehydroascorbate reductase, Synonyms: At5g16705/At5g16710	0.66	1.11
At2g39770	VTC1-1 (ascorbate (vitamin C) biosynthesis, GDP-mannose pyrophosphorylase/ mannose-1-pyrophosphatase. This enzyme provides GDP-mannose, which is used for cell wall carbohydrate biosynthesis and protein glycosylation as well as for ascorbate (vitamin C) biosynthesis	0.93	1.42
At5g28840	ATGME (ascorbate biosynthesis Protein with GDP-D-mannose 3',5'-epimerase activity. . It catalyzes the conversion of GDP-D-mannose to GDP-L-galactose.	0.99	0.93
At3g02870	VTC4-1L-ascorbic acid biosynthetic process,inositol or phosphatidylinositol phosphatase activity, sulfur metabolic process, L-galactose-1-phosphate phosphatase activity inositol monophosphatase family protein [Arabidopsis thaliana] (TAIR:At1g31190.1); similar to L-galactose-1-phosphate phosphatase [Malus x domestica] (GB:AAV49507.1); contains InterPro domain Inositol monophosphatase (InterPro:IPR000760)	0.89	1.13
At4g33670	L-GalDH (L-galactose dehydrogenase (L-GalDH), identical to L-galactose dehydrogenase (Arabidopsis thaliana) GI:16555790; similar to L-fucose dehydrogenase (Pseudomonas sp.) GI:829054; contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family	0.78	1.14
At3g47930	AtGLDH(L-galactono-1,4-lactone dehydrogenase, putative, strong similarity to L-galactono-1,4-lactone dehydrogenase, Brassica oleracea, Z97060 (gi:2760543), and gi:3986289 from Ipomea batatas	0.84	0.86
At2g46750	L-Gloli-like-3 (FAD-binding domain-containing protein, low similarity to SP P58710 L-gulonolactone oxidase (EC 1.1.3.8) {Mus musculus}; contains Pfam profile PF01565: FAD binding domain	0.78	0.79
At5g56490	L-GLOLIlike7 (FAD-binding domain-containing protein, strong similarity to At1g32300, At2g46740, At2g46750, At2g46760; contains PF01565: FAD binding domain	0.89	1.08
At1g55920	chloroplast/cytosol localized serine O-acetyltransferase involved in sulfur assimilation and cysteine biosynthesis. Expressed in the vascular system.	0.98	1.32
At2g17640	cytosolic serine O-acetyltransferase involved in sulfur assimilation and cysteine biosynthesis. Expressed in the vascular system. Expression is induced after long-term sulfur starvation.	1.58	1.15
At3g13110	mitochondrial serine O-acetyltransferase involved in sulfur assimilation and cysteine biosynthesis. Expressed in the vascular system.	1.56	1.07
At4g35640	ATSERAT2;1 (cytosolic serine O-acetyltransferase involved in sulfur assimilation and cysteine biosynthesis. Expressed in the vascular system. Expression is induced in both roots and shoots under sulfur-	0.98	2.40

	starved conditions.		
At5g56760	ATSERAT1;1 (cytosolic serine O-acetyltransferase involved in sulfur assimilation and cysteine biosynthesis. Expressed in the vascular system.	0.88	1.44
At1g32210	DAD-1 (defender against, involved in suppression of apoptosis. Complements a mammalian apoptosis suppressor mutation.	0.89	1.00
At4g20380	LSD1 (monitors a superoxide-dependent signal and negatively regulates a plant cell death pathway. contains zinc-finger motifs. LSD1 negatively regulates a basal defense pathway that can act upstream or independently of both NIM1/NPR1 function and SA accumulation following avirulent or virulent pathogen challenge	0.96	1.10
At3g44880	ACD1 (Pheide a oxygenase (PAO). Accelerated cell death (acd1) mutants show rapid, spreading necrotic responses to both virulent and avirulent Pseudomonas syringae pv. maculicola or pv. tomato pathogens and to ethylene.	0.88	1.65
At5g43060	SAG12 (cysteine proteinase, putative / thiol protease, putative, similar to cysteine proteinase RD21A precursor (thiol protease) GI:435619, SP:P43297 from (Arabidopsis thaliana)	0.93	1.18
At3g02040	SRG (glycerophosphoryl diester phosphodiesterase family protein, contains Pfam profile PF03009: Glycerophosphoryl diester phosphodiesterase family	0.90	0.99
At4g35770	SAP (senescence-associated gene that is strongly induced by phosphate starvation	0.56	0.74
At5g47120	ATBI-1(homolog of mammalian Bax inhibitor 1. Bax-induced cell death can be downregulated by ectopically expressing AtBI in planta. In human fibrosarcoma cells, cell death is INDUCED by AtBI-1, suggesting that it might act as a dominant inhibitor of the endogenous mammalian BI-1. Localization assays were done in mammalian cells.	0.80	1.04
At5g23040	CDF-1(Cell growth defect factor 1.Causes Bax mediated lethality in yeast by generating reactive oxygen species and this effect is suppressed by AtBI-1.	0.83	1.36
At1g07940	EF-1 (elongation factor 1-alpha / EF-1-alpha, mitochondrion, calmodulin binding, translation elongation factor activity, translational elongation identical to GB:CAA34456 from (Arabidopsis thaliana) (Plant Mol. Biol. 14 (1), 107-110 (1990))	2.04	0.62
At2g01010	18SrRNA cytosolic small ribosomal subuni	1.00	1.30
At5g44340	tubulin4 (Tubulin beta-4 chain (TUB4), nearly identical to SP P24636 Tubulin beta-4 chain {Arabidopsis thaliana}	0.94	1.24
At1g49240	Actin 8 (Member of a subclass of actins composed of ACT2 and ACT8. Its mRNA is strongly expressed in strongly expressed in leaves, roots, stems, flowers, pollen, and siliques. However, protein expression, assayed by a ACT8:GUS fusion reporter, is very low in pollen.	0.87	1.18
At3g02470	SAMDC (adenosyl-methionine decarboxylase activity, polyamine biosynthetic process	1.06	0.88

At2g16500	ADC1 (arginine decarboxylase (ADC), a rate-limiting enzyme catalyzes the first step of polyamine (PA) biosynthesis	0.90	1.09
At4g34710	ADC2 (arginine decarboxylase (ADC), a rate-limiting enzyme that catalyzes the first step of polyamine (PA) biosynthesis via ADC pathway in Arabidopsis thaliana. Arabidopsis genome has two ADC paralogs, ADC1 and ADC2. ADC2 is stress-inducible (osmotic stress). Double mutant analysis showed that ADC genes are essential for the production of PA, and are required for normal seed development. Overexpression causes phenotypes similar to GA-deficient plants and these plants show reduced levels of GA due to lower expression levels of AtGA20ox1, AtGA3ox3 and AtGA3ox1	0.93	1.06
At1g23820	SPDS (spermidine synthase 1 (SPDSYN1) / putrescine aminopropyltransferase 1, identical to SP Q9ZUB3 Spermidine synthase 1 (EC 2.5.1.16) (Putrescine aminopropyltransferase 1) (SPDSY 1) {Arabidopsis thaliana}	0.86	1.02
At5g14040	MPT1 (mitochondrial phosphate transporter, identical to mitochondrial phosphate transporter Gl:3318617 from (Arabidopsis thaliana)	0.88	0.89
At3g08580	ANT1 (ADP, ATP carrier protein 1, mitochondrial / ADP/ATP translocase 1 / adenine nucleotide translocator 1 (ANT1), identical to SWISS-PROT:P31167 ADP,ATP carrier protein 1 (Adenine nucleotide translocator 1) (Arabidopsis thaliana)	0.92	0.90
At5g46110	TPT (phosphate/triose-phosphate translocator, putative, identical to phosphate/triose-phosphate translocator precursor (Arabidopsis thaliana)	0.75	0.72
At4g00860	ATOZ11 (putative pathogenesis-related protein whose transcript level is induced in response to ozone and pathogenic Pseudomonas strains.	0.93	1.54
At5g40650	SDH2 (iron-sulfur component of the succinate dehydrogenase complex, a component of the mitochondrial respiratory chain complex II. The product of the nuclear encoded gene is imported into the mitochondrion. Expressed during germination and post-germinative growth.	1.50	1.17
At5g66760	SDH1(flavoprotein subunit of the mitochondrial succinate dehydrogenase complex.	1.41	0.93
At1g77120	ADH1(Catalyzes the reduction of acetaldehyde using NADH as reductant. Requires zinc for activity. Dimer. Anaerobic response polypeptide (ANP). Fermentation.	0.83	1.30
At5g13110	G6PD (glucose-6-phosphate dehydrogenase (G6PDH),In green tissues of plants under illumination, photosynthesis is the primary source of reduced nicotinamide adenine dinucleotide phosphate (NADPH), which is utilized in reductive reactions such as carbon fixation and nitrogen assimilation. In non-photosynthetic tissues or under non-photosynthetic conditions, the oxidative pentose phosphate pathway contributes to basic metabolism as one of the major sources of NADPH. The first and committed reaction is catalyzed by glucose-6-phosphate dehydrogenase (G6PDH).	0.87	1.18
At5g65430	14-3-3s (The major native forms of 14-3-3s are homo- and hetero-dimers, the biological functions of which are to interact physically with specific client proteins and thereby effect a change in the client. As a result, 14-3-3s are involved in a vast array of processes such as the response to stress, cell-	0.99	1.29

	cycle control, and apoptosis, serving as adapters, activators, and repressors. There are currently 133 full-length sequences available.		
At4g37980	ELI3-1(mannitol dehydrogenase.	0.84	1.08
At3g21720	ICL (isocitrate lyase, putative, similar to isocitrate lyase GI:167144 from (Brassica napus)	1.06	1.10
At1g21250	WAK1 (cell wall-associated kinase, may function as a signaling receptor of extracellular matrix component.	0.96	1.14
At5g20230	BCB (Al-stress-induced gene	0.96	1.54
At5g20280	SPS (sucrose-phosphate synthase, putative, similar to sucrose-phosphate synthase	0.65	0.88
At5g20830	SUS1 (sucrose synthase 1	0.79	1.23
At3g13790	BFS-1 (beta-fructosidase (BFRUCT1) / beta-fructofuranosidase / cell wall invertase, identical to beta-fructofuranosidase GI:402740 from (Arabidopsis thaliana)	0.78	1.51
At1g22710	SUC2 (high-affinity transporter essential for phloem loading and long-distance transport. A major sucrose transporter, AtSUC2 can also transport a wide range of physiological and synthetic glucose conjugates with both α - or β -linkage.	1.22	0.99
At3g50970	LTI3 (dehydrin xero2 (XERO2) / low-temperature-induced protein LTI30 (LTI30), identical to dehydrin Xero 2 (Low-temperature-induced protein LTI30) (Arabidopsis thaliana) SWISS-PROT:P42758	1.07	1.16
At1g20450	LTI29 (gene induced by low temperature and dehydration.	0.94	1.57
At1g42990	AtbZIP60 (bZIP DNA binding domain followed by a putative transmembrane domain. GFP fusions containing the first 260 amino acids (AtbZIP60deltaC) are nuclear-localized. AtbZIP60 is upregulated by the addition of tunicamycin (ER stress response inducer), DTT (inhibitor of disulfide bond formation) and azetin-2-carboxylate (proline analog perturbing protein structure). It is hypothesized that upon ER stress the protein is proteolyzed and the soluble part translocated into the nucleus. AtbZIP60deltaC can activate the promoters of the ER chaperones BiP1, BiP2 and BiP3 and CNX1 and CNX2 via binding to the ER stress response element (ERSE) and the plant unfolded protein response element(P-UPRE). It can also activate its own transcription.	0.95	1.44
At5g42020	BiP-2 (luminal binding protein 2 (BP2), similar to SWISS-PROT: Q39043; GI:1303695; luminal binding protein (BiP) (Arabidopsis thaliana)	1.43	0.37
At5g28540	BiP1 (luminal binding protein 1 (BiP-1) (BP1), SWISS-PROT:Q9LKR3 PMID:8888624	1.29	0.34
At4g24190	HSP90 (ER-resident HSP90-like protein and is involved in regulation of meristem size and organization. Single and double mutant analyses suggest that SHD may be required for the correct folding and/or complex formation of CLV proteins. Lines carrying recessive mutations in this locus exhibits expanded shoot meristems, disorganized root meristems, and defective pollen tube elongation. Transcript is detected in all tissues examined and is	1.19	0.61

	not induced by heat.		
At5g56030	HSP81-2 (heat shock protein 90 (HSP90) gene family. Expressed in all tissues and abundant in root apical meristem, pollen and tapetum. Expression is NOT heat-induced but induced by IAA and NaCl.	1.05	0.68
At2g45770	SRPS (signal recognition particle receptor protein, chloroplast (FTSY), similar to Cell division protein ftsY homolog (SP:O67066) {Aquifex aeolicus}; contains Pfam PF00448: SRP54-type protein, GTPase domain contains TIGRFAM TIGR00064: signal recognition particle-docking protein FtsY contains Pfam PF02881: SRP54-type protein, helical bundle domain; identical to cDNA chloroplast FtsY homolog GI:4583547	0.95	0.98
At2g34250	Sec61 α (protein transport protein sec61, putative, similar to PfSec61 (Plasmodium falciparum) GI:3057044; contains Pfam profile PF00344: eubacterial secY protein	0.69	1.05
At2g45070	Sec61 β (beta family protein, similar to SP P52870 Protein transport protein SEC61 beta 1 subunit {Saccharomyces cerevisiae}; contains Pfam profile PF03911: Sec61beta family	0.87	0.90
At2g47470	PDIL (protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily	0.99	1.02
At3g54960	PDIL2 (protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	0.96	1.18
At1g08450	CRT3 (calreticulin 3 , identical to similar to SP O04153 Calreticulin 3 precursor {Arabidopsis thaliana}	1.43	0.85
At1g09210	CRT2 (calreticulin 2, identical to SP Q38858 Calreticulin 2 precursor {Arabidopsis thaliana}	0.87	0.97
At1g56340	CRT1 (calreticulin 1 , identical to calreticulin (crt1) GI:2052379 (Arabidopsis thaliana)	1.14	1.04
At5g61790	CNX1 (calnexin 1, identical to calnexin homolog 1, Arabidopsis thaliana, EMBL:AT08315 (SP P29402	0.93	1.41
At5g07340	CNX2 (calnexin, putative, identical to calnexin homolog 2 from Arabidopsis thaliana (SP Q38798), strong similarity to calnexin homolog 1, Arabidopsis thaliana, EMBL:AT08315 (SP P29402); contains Pfam profile PF00262 calreticulin family	0.75	1.36
At2g01720	RBP (ribophorin I family protein, similar to SP P04843 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor (EC 2.4.1.119) (Ribophorin I) {Homo sapiens}; contains Pfam profile PF04597: Ribophorin I	0.95	0.97
At4g22670	TTR (tetratricopeptide repeat (TPR)-containing protein, similar to Hsc70-interacting protein (Hip) from {Homo sapiens} SP P50502, {Rattus norvegicus} SP P50503; contains Pfam profile PF00515: tetratricopeptide repeat (TPR) domain	1.17	0.80
At2g47320	CCP (peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein, contains Pfam domain, PF00160: peptidyl-prolyl cis-trans isomerase,	1.03	0.99

	cyclophilin-type		
At1g14010	TTP (emp24/gp25L/p24 family protein, similar to SP P49755 Transmembrane protein Tmp21 precursor (21 kDa Transmembrane trafficking protein) {Homo sapiens}; contains Pfam profile PF01105: emp24/gp25L/p24 family	0.81	0.95
At5g03280	EIN2 (ethylene-insensitive 2 (EIN2), identical to EIN2 (Arabidopsis thaliana) gi 5231113 gb AAD41076; member of the natural resistance-associated macrophage protein (NRAMP) metal transporter family, PMID:11500563; metal transport capacity has not been shown, PMID:11500563, PMID:1038174	0.80	1.01
At5g16710	chlDHAR (chloroplastic dehydroascorbate reductase	1.04	1.19
At4g30570	EIN21-c (GDP-mannose pyrophosphorylase, putative, similar to GDP-mannose pyrophosphorylase (Arabidopsis thaliana) GI:3598958; contains Pfam profile PF00483: Nucleotidyl transferase	0.80	1.47
At5g21105	AO (L-ascorbate oxidase, putative, similar to L-ascorbate oxidase from {Nicotiana tabacum} SP Q40588, {Cucurbita pepo var. melopepo} SP P37064; contains Pfam profile PF00394: Multicopper oxidase; supported by cDNA gi_15215753_gb_AY050406.1_; A false intron was added between exons 4 and 5 to circumvent the single nucleotide insertion in this BAC which, otherwise, causes a frameshift.	0.86	1.43

Supplemental Table 4. Quantification of Northern blot and Semiquantitative RT-PCR

Mean pixel number at preset intensity threshold						
Northern				Semiquantitative RT-PCR		
Pin2	Spin + Se	118		GSH2	Spin + Se	87
Pin3	Spin - Se	144		GSH2	Spin - Se	86
Pin4	Salb + Se	15		GSH2	Salb + Se	52
Pin5	Salb - Se	11		GSH2	Salb - Se	74
AOS	Spin + Se	83		GSH1	Spin + Se	48
AOS	Spin - Se	89		GSH1	Spin - Se	47
AOS	Salb + Se	5		GSH1	Salb + Se	46
AOS	Salb - Se	0		GSH1	Salb - Se	5
PDF1.2	Spin + Se	213		SAT52	Spin + Se	83
PDF1.2	Spin - Se	182		SAT52	Spin - Se	91
PDF1.2	Salb + Se	24		SAT52	Salb + Se	62
PDF1.2	Salb - Se	49		SAT52	Salb - Se	12
Cys synthase	Spin + Se	137		SAT1	Spin + Se	90
Cys synthase	Spin - Se	156		SAT1	Spin - Se	129
Cys synthase	Salb + Se	152		SAT1	Salb + Se	59
Cys synthase	Salb - Se	35		SAT1	Salb - Se	42
SAT 52	Spin + Se	207		APS	Spin + Se	111
SAT 52	Spin - Se	142		APS	Spin - Se	35
SAT 52	Salb + Se	101		APS	Salb + Se	103

SAT 52	Salb - Se	69		APS	Salb - Se	124
EF1 α	Spin + Se	73		Pin2	Spin + Se	84
EF1 α	Spin - Se	127		Pin2	Spin - Se	101
EF1 α	Salb + Se	133		Pin2	Salb + Se	74
EF1 α	Salb - Se	143		Pin2	Salb - Se	57
18s rRNA	Spin + Se	144		PR1	Spin + Se	59
18s rRNA	Spin - Se	151		PR1	Spin - Se	82
18s rRNA	Salb + Se	143		PR1	Salb + Se	0
18s rRNA	Salb - Se	133		PR1	Salb - Se	0
				ACS6	Spin + Se	26
				ACS6	Spin - Se	61
				ACS6	Salb + Se	8
				ACS6	Salb - Se	5
				EF1 α	Spin + Se	144
				EF1 α	Spin - Se	148
				EF1 α	Salb + Se	163
				EF1 α	Salb - Se	132

Supplemental Table 5. Arabidopsis primers
<p>Sultr2;1 (At5g10180)</p> <p>Forward: 5'-<u>aagcttgatcctcaatatggc</u>-3'</p> <p>Reverse: 5'-<u>ccatcccataatccttctc</u>-3'</p>
<p>ACS6 (At4g11280)</p> <p>Forward: 5'-<u>taagcttagtgacacgag</u></p> <p>Reverse: <u>gtatctcatgtaatttaac</u>-3'</p>
<p>PIN2 (At2g02100)</p> <p>Forward: 5'-<u>tctatgcgttgatctcagc</u></p> <p>Reverse: <u>cgttgcttctgcaccagacattgc</u>-3'</p>
<p>APS1 (At3g22890)</p> <p>Forward: 5'-<u>tactcgtaggagacttcttgag</u></p> <p>Reverse: <u>catatgacaagacgcaaggcaa</u>-3'</p>
<p>SAT52 (At5g56760)</p> <p>Forward: 5'-<u>tatggacacaatcacggaagc</u></p> <p>Reverse: <u>ctcggaatggtcagattacatc</u>-3'</p>
<p>GSH1 (At4g23100)</p>

Forward: 5'- acatcgactgtactggaatgac
Reverse: gttcgaagagctgctgtactaa -3'
GSH2 (At5g27380)
Forward: 5'- gaacgcaacatgtacgatcaac
Reverse: gcgtttaccataagcatcaagc -3'

Supplemental Table 6. Percent relatedness by DNA sequence similarities.

Gene name & ID	<i>S.pin</i> vs <i>S.alb</i>	<i>S.pin</i> vs <i>A.thal</i>	<i>S.alb</i> vs <i>A.thal</i>
Sultr2;1 (At5g10180)	84.00	86.00	96.00
PIN2 (At2g02100)	99.00	88.80	88.80
ACS6 (At4g11280)	85.00	79.00	78.00
APS1 (At3g22890)	97.90	92.00	92.00
SAT52 (At5g56760)	98.90	87.10	86.50
GSH1 (At4g23100)	97.40	92.40	92.00
GSH2 (At5g27380)	98.10	89.50	89.70
Average	94.30	87.82	89.00
Standard error	2.54	1.71	2.15